FIG.1

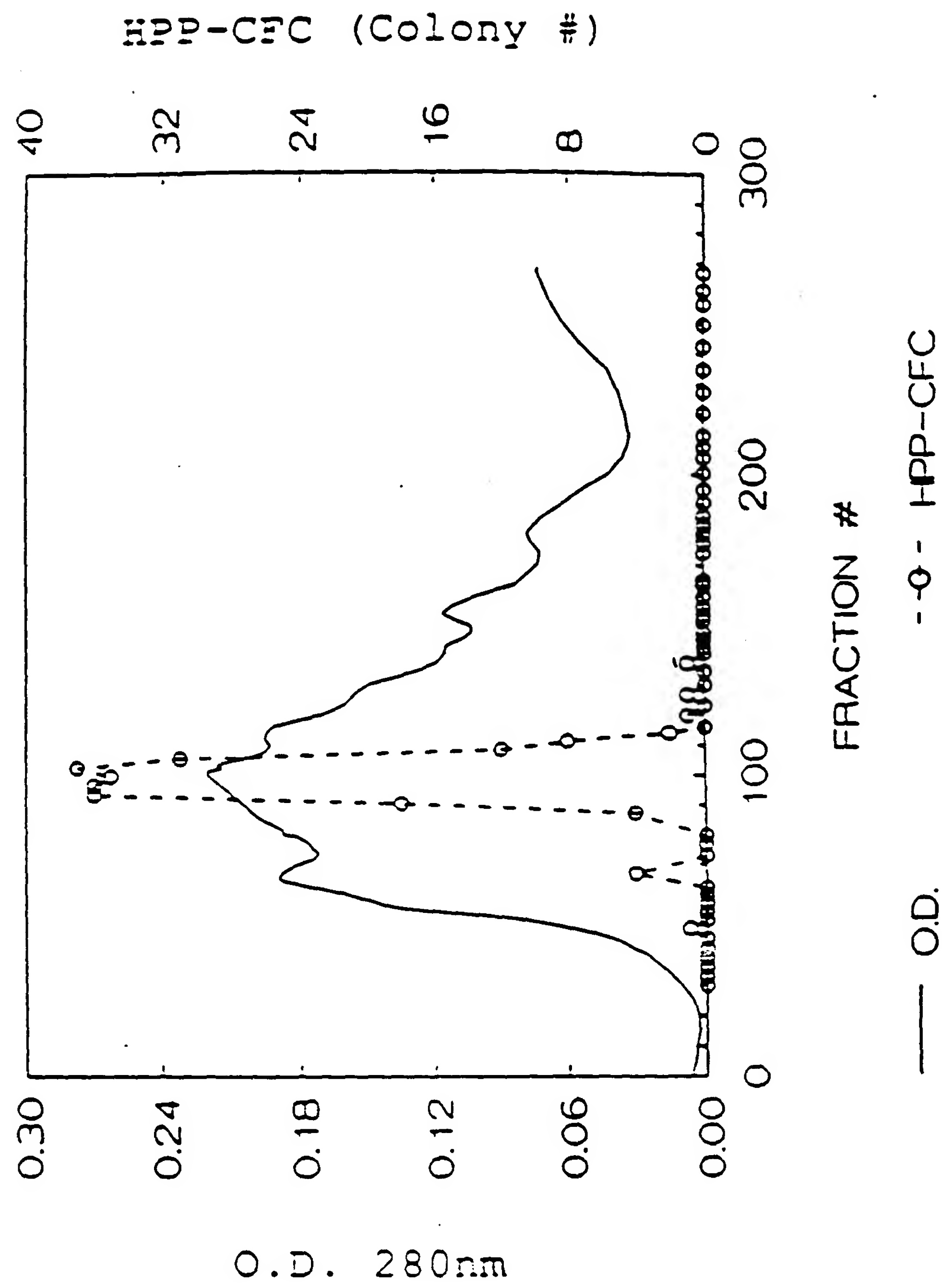

HPP-CFC (Colony #)
40
32
24
16
8
0
0.30
0.24
0.18
0.12
0.06
0.00
0
100
200
300
FRACTION #
— O.D.
-o- HPP-CFC
O.D. 280nm

FIG.2

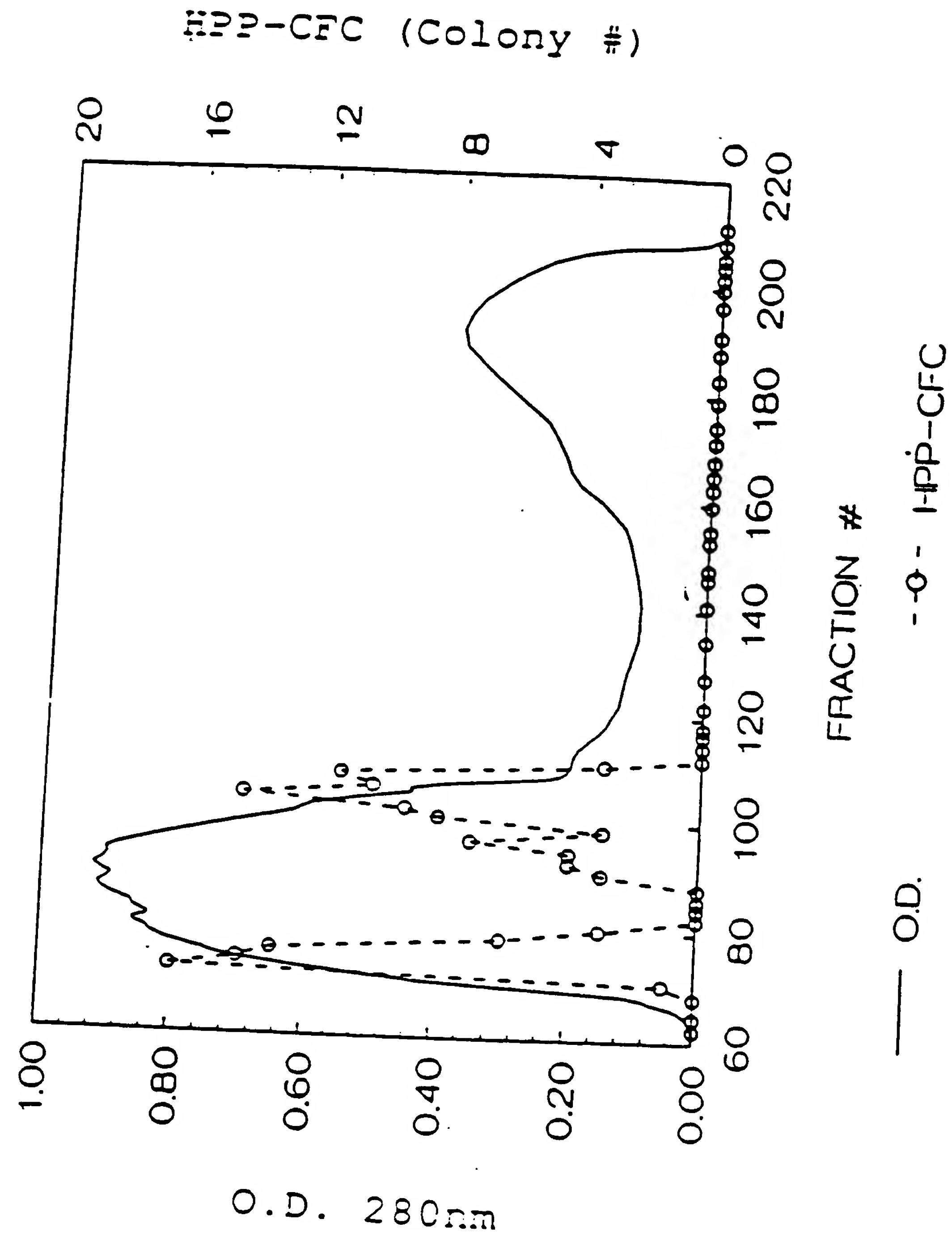

HPP-CFC (Colony #)
20
16
12
8
4
0
1.00
0.80
0.60
0.40
0.20
0.00
O.D. 280nm
60
80
100
120
140
160
180
200
220
FRACTION #
— O.D.
-o- HPP-CFC

FIG.3

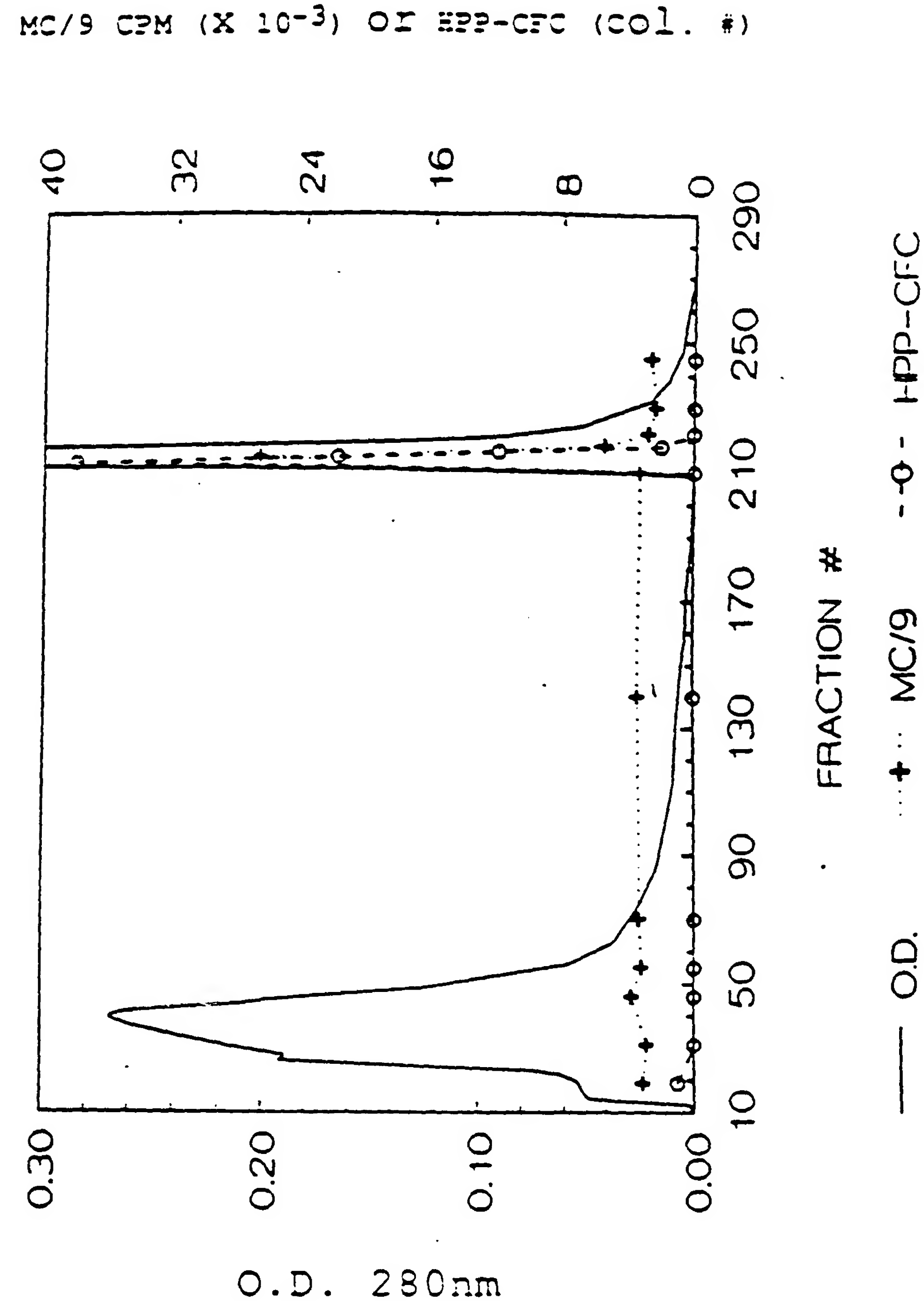
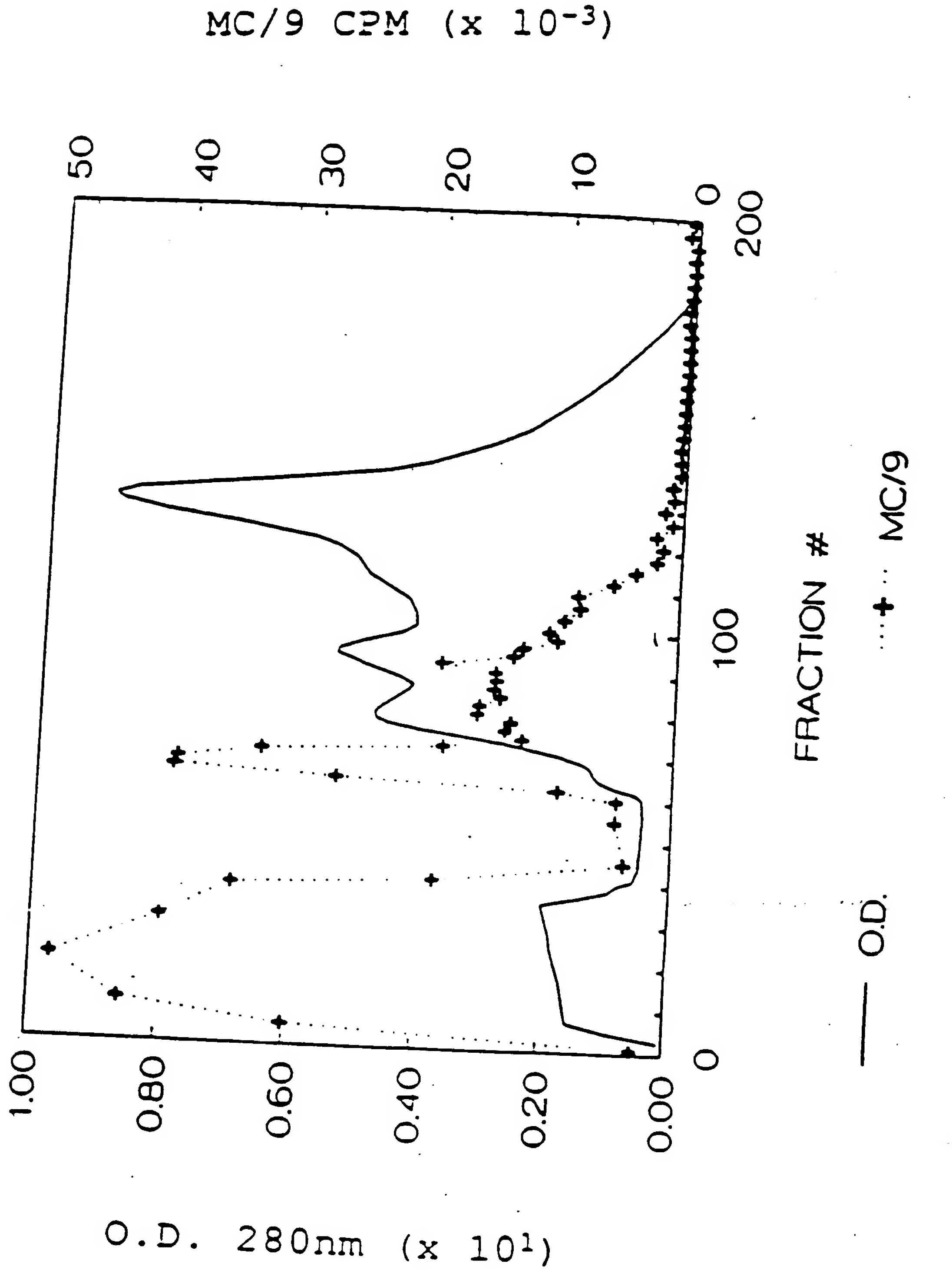

MC/9 CPM (X 10-3) or HPP-CFC (col. #)
40
32
24
16
8
0
0.30
0.20
0.10
0.00
10
50
90
130
170
210
250
290
FRACTION #
O.D.
MC/9
HPP-CFC
O.D. 280nm

FIG. 4



MC/9 CPM (x 10^{-3})
50
40
30
20
10
0
1.00
0.80
0.60
0.40
0.20
0.00
0
100
200
FRACTION #
O.D.
MC/9
O.D. 280nm (x 10^{1})

FIG.5

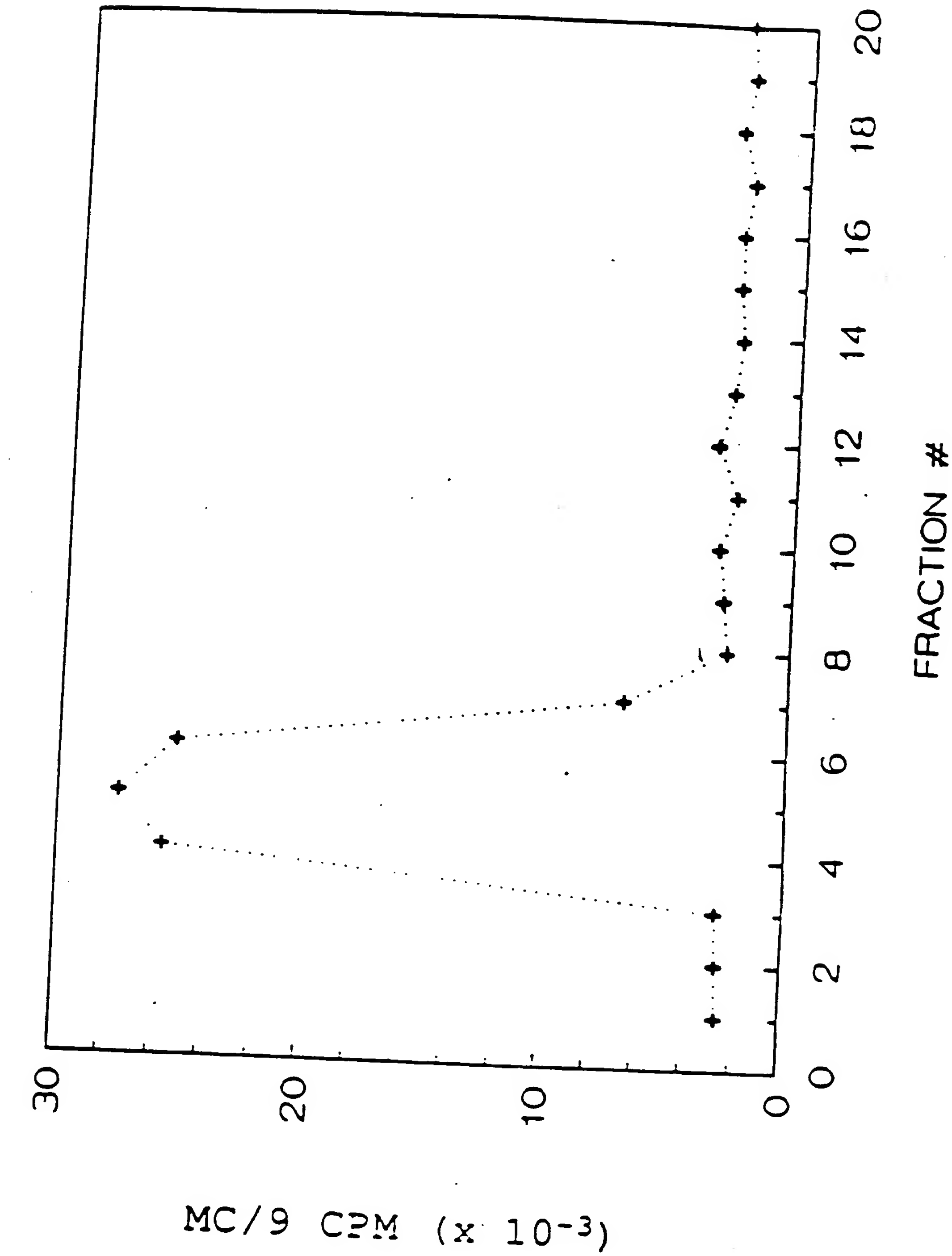


FIG. 6

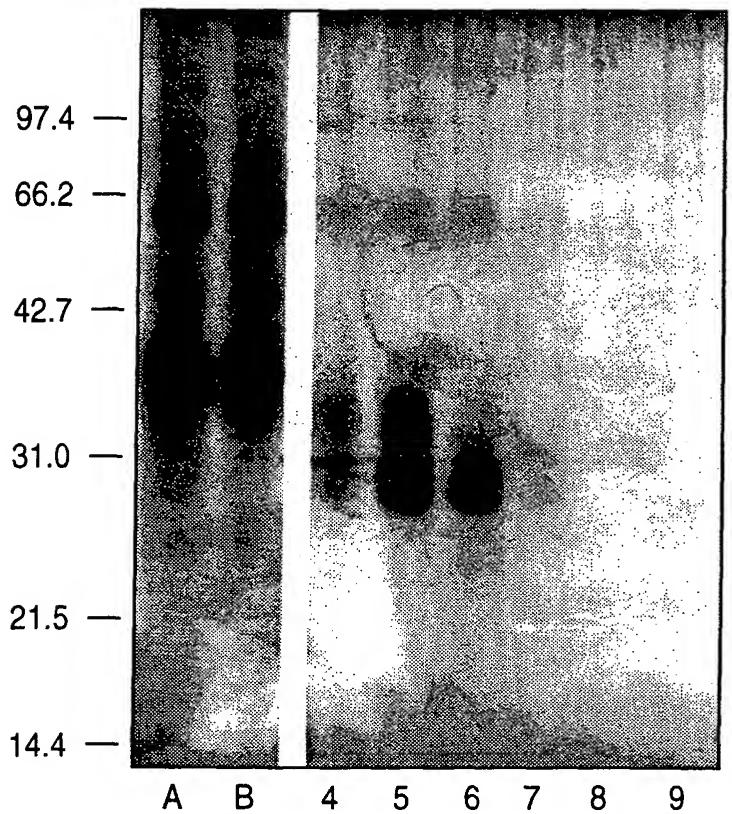


FIG.7

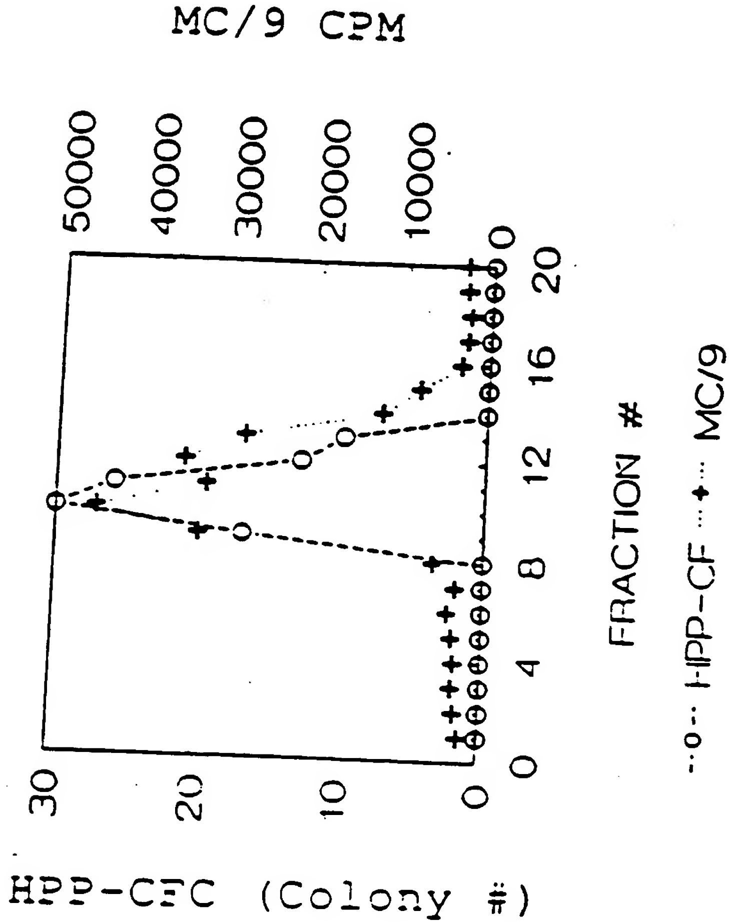

MC/9 CPM
50000
40000
30000
20000
10000
0
30
20
10
0
0
4
8
12
16
20
FRACTION #
--o-- HPP-CF ···+··· MC/9
HPP-CFC (Colony #)

FIG. 8

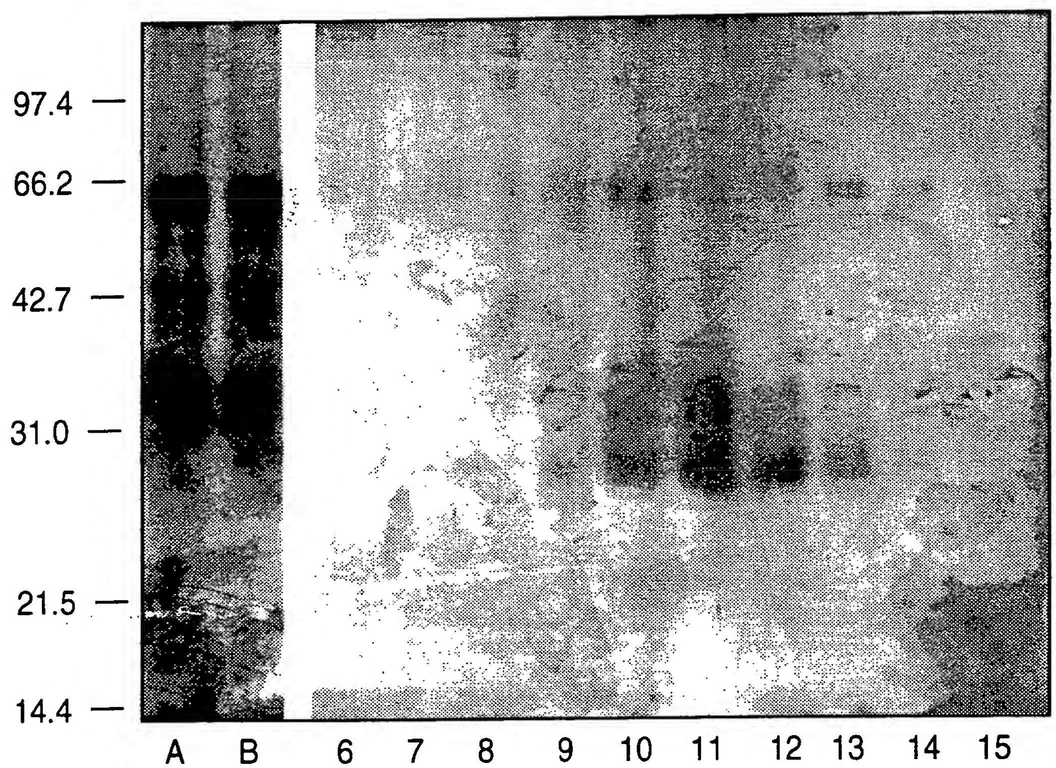
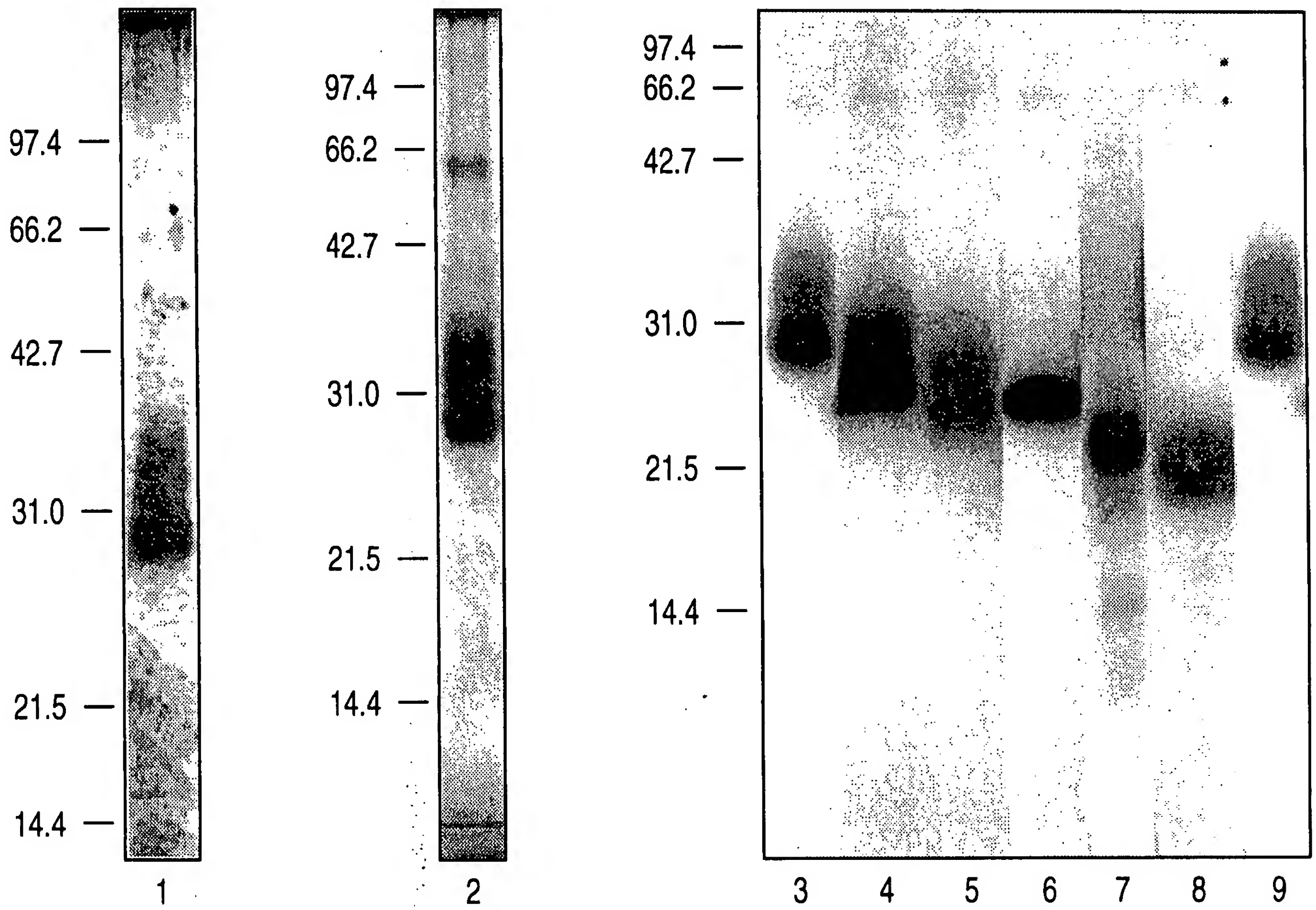


FIG. 9



97.4
66.2
42.7
31.0
21.5
14.4
1
97.4
66.2
42.7
31.0
21.5
14.4
2
97.4
66.2
42.7
31.0
21.5
14.4
3
4
5
6
7
8
9

FIG.10

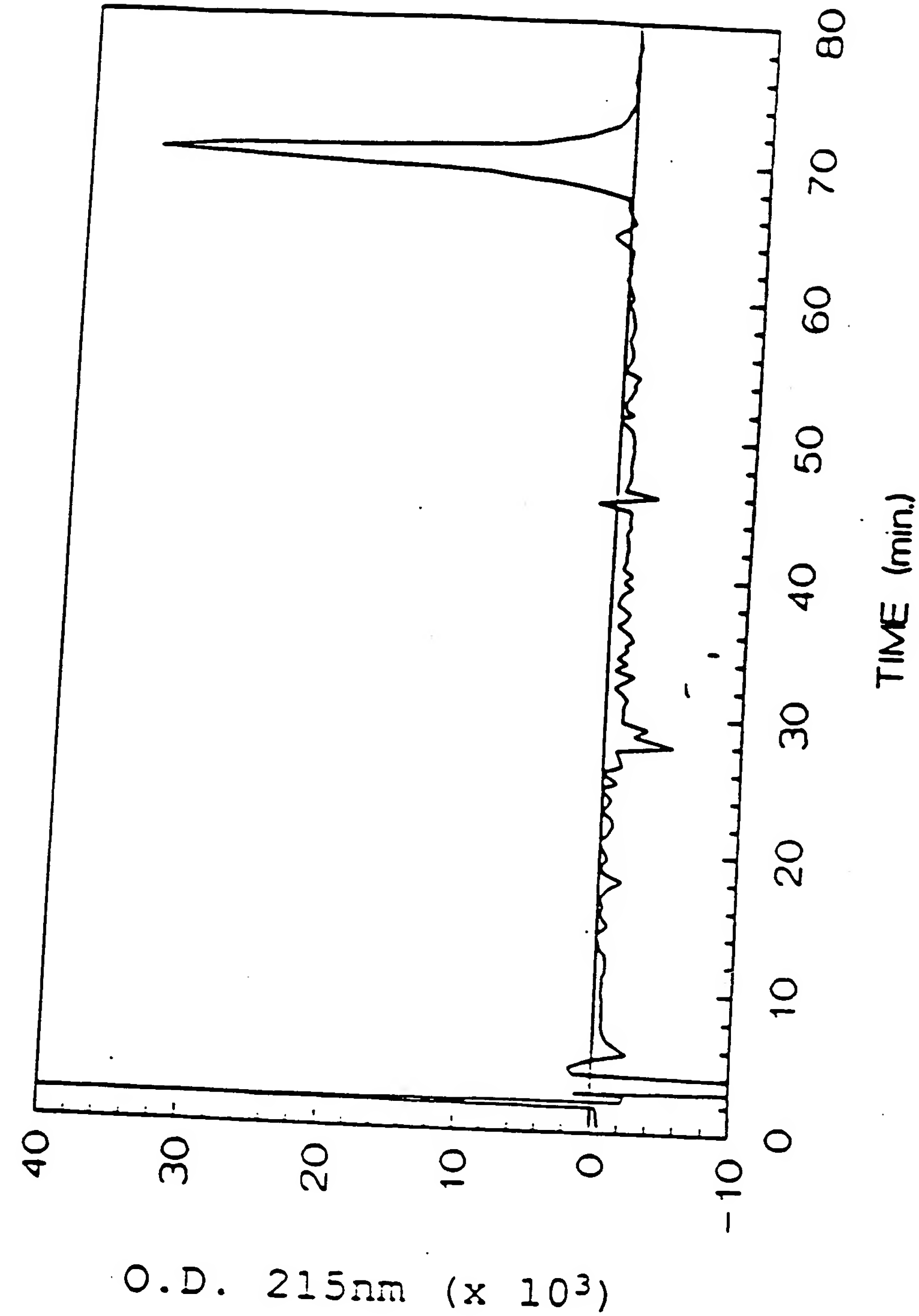


FIG.11

1 10 20

pE E I C R N P V T D N V K D I T K L V A N L P N D

|-- Sequencing after

|-------- T-5a -------

30 40 50

Y M I T L N Y V A G M D V L P S H C W L R D M V T

<Glu Aminopeptidase Treatment -------------->

|-----------------

-- T-5a ----------------|

|--------- CB-6a ---------||-------- CB-8; CB-10 ---------|

60 70

H L S V S L T T L L D K F S **N** I S E G L S **N** Y S I

------ Sequencing after Trp Cleavage ----------------

80 90 100

I D K L G K I V D D L V A C M E E N A P K N V K E

------------------------->

|------------------- T-3 ------------------| ---

|--

|-CB-14;CB-15;CB-16 -

|-------- S-1---------|

110 120

S L K K P E T R **N** F T P E E F F S I F **N** R S I D A

--- T-1 ---------------|---- T-4 (N109 nonglyco) -----||-----------

----- T-7 (N120 glyco); T-8 (N109 nonglyco) -----|

------------------------- CB-14; CB-15; CB-16 -----------------

|----------------- S-5 or S-6 (N109 nonglyco) -----------------

130 140 150

F K D F M V A S D T S D C V L S **S** **T** L G P E K D S

---------------------------- T-5b ------------------------------------

----------------|--------------------------- CB-6B --------------------------

------ S-5 or S-6-----------.

160

R V S V **T** K P F M L P P V A(A)

--||----- T-2 ---| <--- <--- (Carboxypeptidase)

------ CB-6B ----------

------------------ S-2 ----------------------|

FIG.12A

```
OLIGO     SEQUENCE                                LOCATION

219-21    ACATTCTTIGGIGCATTCTCCTCCAT              393-368
            G  T        G  T  T

219-22    AAAAACTCCTCIGGIGTAAAATT                 447-425
            G  T  T        G  G

219-25    GTTTCNGGTTTTTT                          420-407
            C     C  C

219-26    ATGGAAGAAAACGCCCCCAAAAACGT              368-393
               G  G  T        G  T

222-11    CCNAATGATTATATGATAAC                    167-186
               C  C  C     C
                         T

222-12    GGNGGNAACATAAANGGCTT                    566-585
                 G   G     T

223-6     ACCATAAAATCTTTAAAICGATC                 492-470
              G  G  C  G     G

224-24    GTATTTTCAATAGATCCATTGA                  450-471

224-25    CCAACTATGTCGCC                          190-202

224-27    GTAGTCAAGCTGACTGATAAG                   273-253
```

FIG.12A CONT.'

224-28	TAACCAACAATGACTAGGCAA	235-215	
225-31	TTCCAGAGTCAGTGTC	547-562	
227-29	GCGAAGCTTGCCTTTCCTTATGAAGAAGA	16-35	*
227-30	GCGCCGCGGTTACGGTGGTAACATGAAGGGCTTTGTGA	586-561	*
228-30	GATAAATGCAAGTGATAATCC	45-65	
230-25	GCGGTCGACCCGCGGAACTTTAAGTCCATGCAACAC	705-685	*
237-19	CACCCGCGGTTATGCAACAGGGGGTAACATAAATGG	569-592	*
237-20	CACCCGCGGTTAGGCTGCAACAGGGGGTAACATAAA	572-595	*

FIG.12B

OLIGO	SEQUENCE	LOCATION
231-27	CTTAATGTTGAAGAAACC	703-686
233-13	GATGGTAGTACAATTGTCAGAC	410-431
233-14	GTCTGACAATTGTACTACCATC	431-410
235-29	CAATTTAGTGACGTCTTTTACA	302-323
235-30	TTAGATGAGTTTTCTTTCACGCAC	556-533
235-31	AAATCATTCAAGAGCCCAGAACCC	566-589
236-31	AACATCCATCCCGGGGAC	366-383
238-31	CTGGCAATATTTTAAGTCTCAAGAAGACC	
241-6	GCGCCGCGGCTCCTATAGGTGCTAATTGG	
254-9	CCTCACCACTGTTTGTGCTGGATCGCA	153-179
262-13	GGTGTCTAGACTTGTGTCTTCTTCATAAGGA	209-190

FIG.12C

OLIGO	SEQUENCE
201-7	CCCCCCCCGG T A
220-3	TTTTTTTTTTTTTTTTTTGG
220-7	TTTTTTTTTTTTTTTTTTAG
220-11	TTTTTTTTTTTTTTTTTTCG
221-11	TTCGGCCGATCAGGCCCCCCCCCC
221-12	TTCGGCCGGATAGGCCTTTTTTTTTTTTTT
228-28	GGCCGGATAGGCCTCACNNNNNNT
228-29	GGCCGGATAGGCCTCAC

FIG.13A

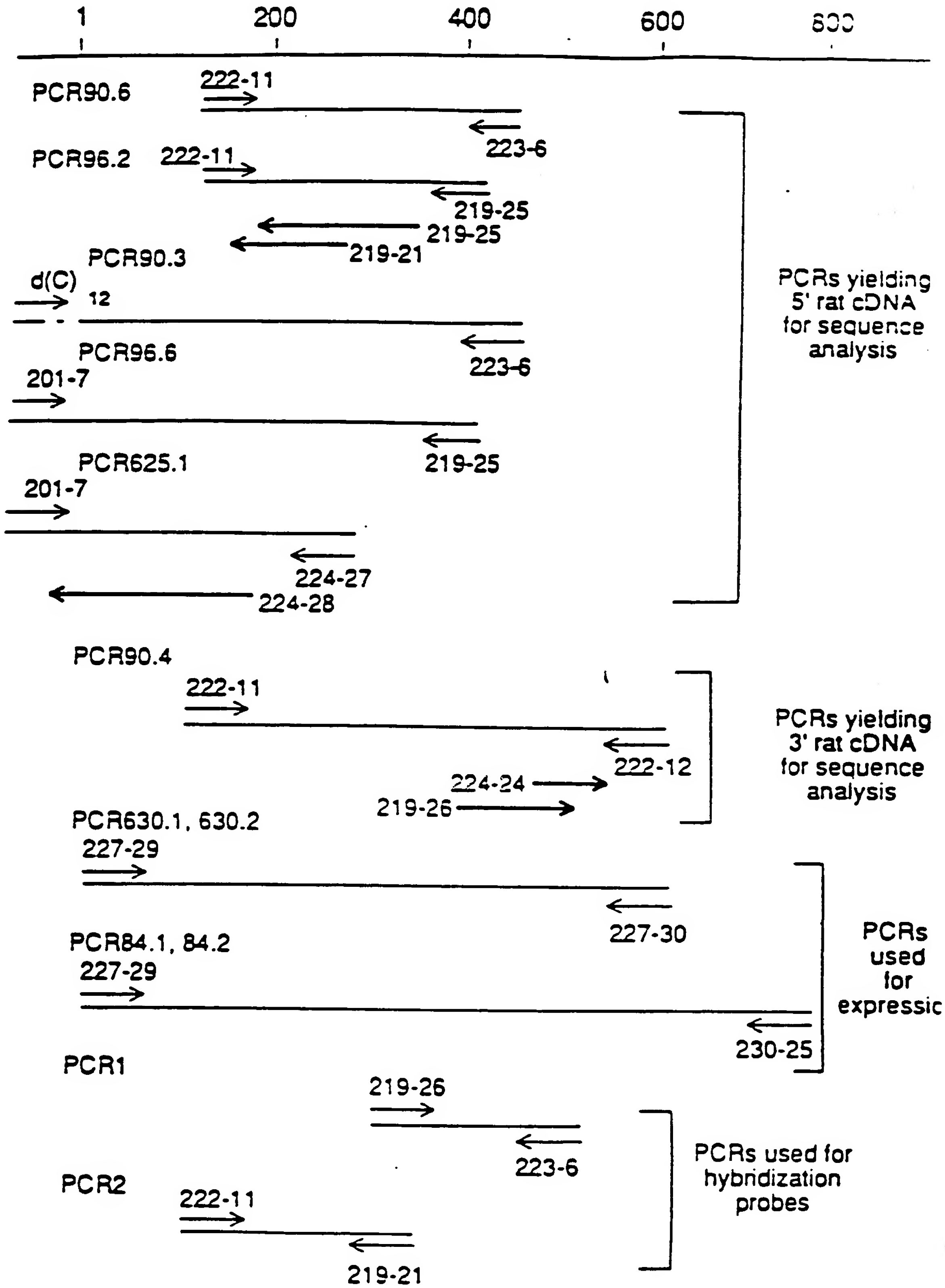

1
200
400
600
800
PCR90.6
222-11
223-6
PCR96.2
222-11
219-25
219-25
219-21
PCR90.3
d(C)
12
223-6
PCR96.6
201-7
219-25
PCR625.1
201-7
224-27
224-28
PCRs yielding 5' rat cDNA for sequence analysis
PCR90.4
222-11
222-12
224-24
219-26
PCRs yielding 3' rat cDNA for sequence analysis
PCR630.1, 630.2
227-29
227-30
PCR84.1, 84.2
227-29
230-25
PCRs used for expressic
PCR1
219-26
223-6
PCR2
222-11
219-21
PCRs used for hybridization probes

FIG. 13B

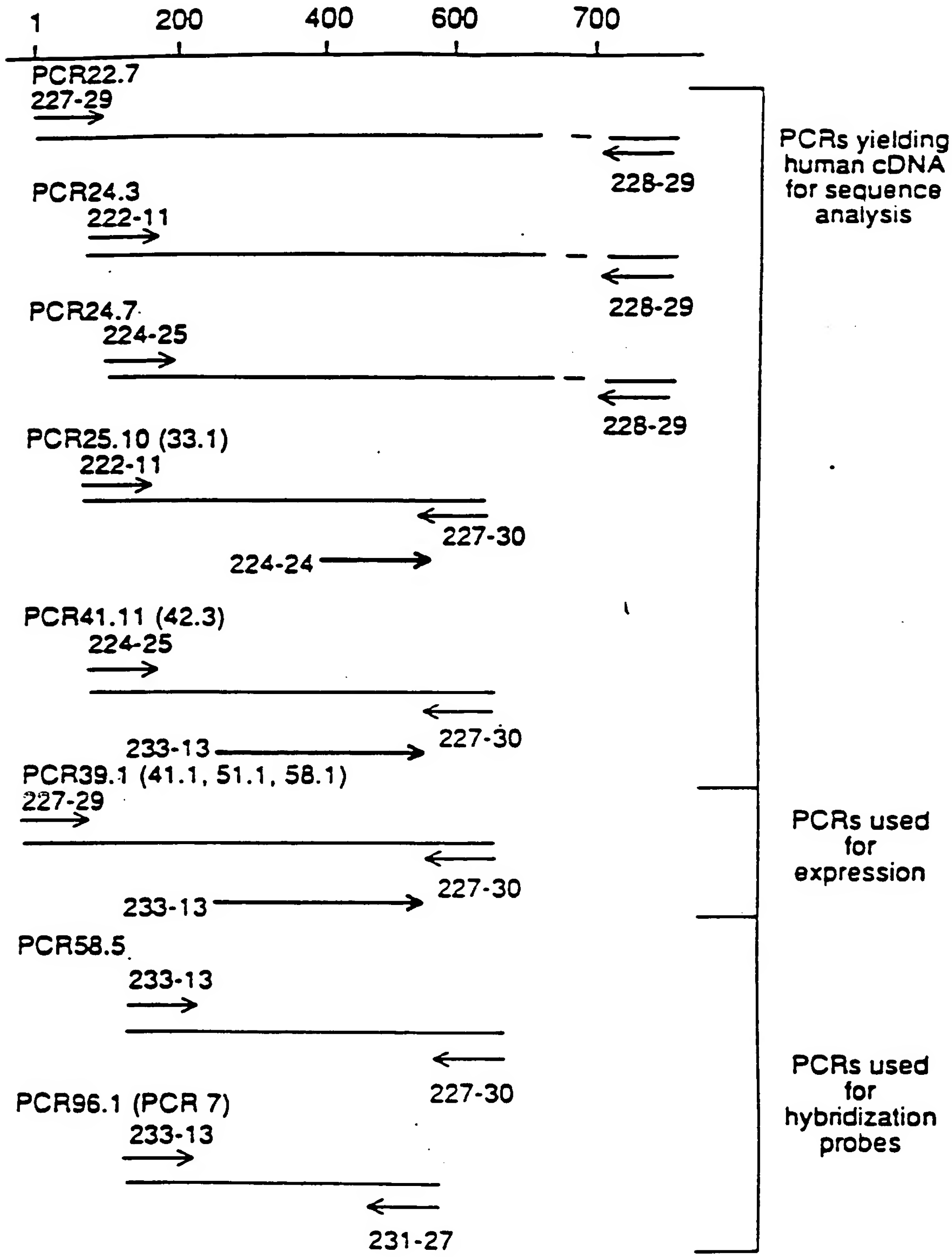

1
200
400
600
700
PCR22.7
227-29
228-29
PCR24.3
222-11
228-29
PCR24.7
224-25
228-29
PCR25.10 (33.1)
222-11
227-30
224-24
PCR41.11 (42.3)
224-25
227-30
233-13
PCR39.1 (41.1, 51.1, 58.1)
227-29
227-30
233-13
PCR58.5
233-13
227-30
PCR96.1 (PCR 7)
233-13
231-27
PCRs yielding human cDNA for sequence analysis
PCRs used for expression
PCRs used for hybridization probes

FIG.14A

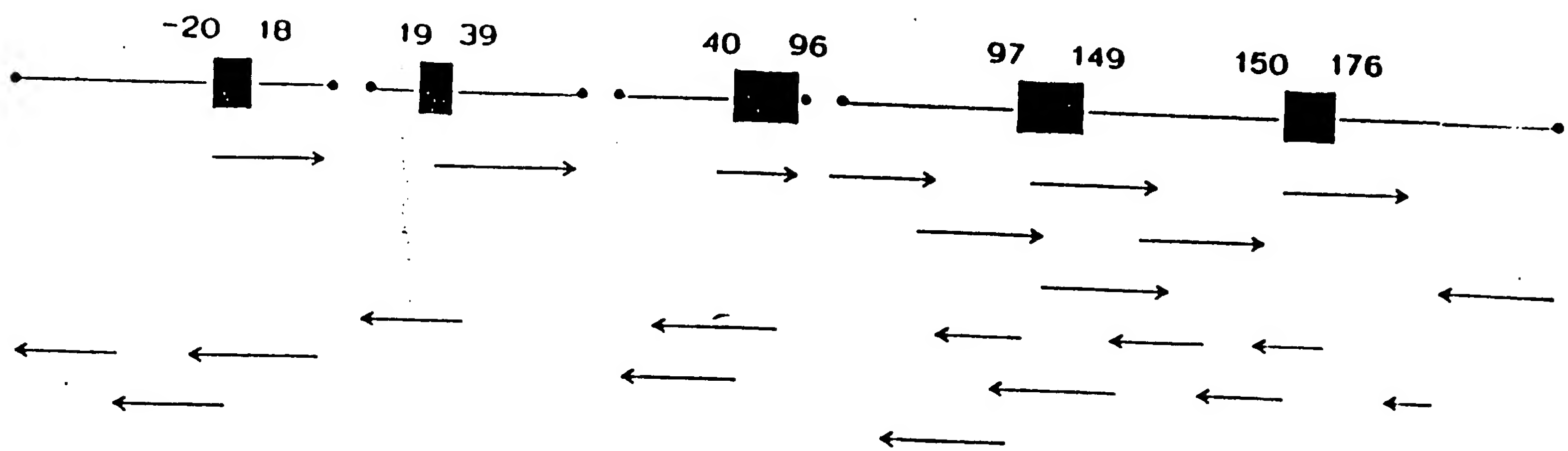


FIG.14B

```
AAAGTATCTTTCTATTGGCGAAGGACATGTTTTCCcATAAGTGGT    45

AAACAnACTGTCTGCACATAATAATTATCTTGCTGCCGTAAAGAT    90

TAGGTTAAATTCTGcCTTCGATCTAAAAACACACCCTTCTGTCAA    135

TCCGAGGAGCAGTGTGCTAGTCTAGAGGTCTAAATGAAGGCTCCT    180

TTCACGGTTGTATTTCTGCTCCCCAAATTGTCCACATTTAAAAGG    225

AGAGTGCTTCTTTTCAGCCTTAGGCTCTGAATTTCATGCATTCCT    270

CCATTTTCCGAGGTCCCccCcAAGTGATAATTCTGTTACACGTTG    315

CTACAAGTTCATCCCTAATTGCCGTCAAGAAACTGACTGTAGAAG    360

GCTTACCACAGACGTTGTAACCGACAGTAAAGCCATTGAAAGAGT    405

AATTCAAACAGGATGGAAGCCAGGAGTATTTTGTGGCTGTTGCTC    450

TTTTTCTTTTCAGTTTGGTGAGAGCAGCTTGAATGCTTAACATTT    495

AAGCCATCAGCTTAAAACAAAACAAAACAAAACAAAAAAAAACCC    540

CGCTCTGGCATATTTGCACTTAACACATACGGTATAAGGTGTTAC    585

TGGTTTGCATAGTTCTGGATTTTTTTTTTTTAAAAACTGATGGAC    630

                                     -20
                                     ThrTrpIleIleThrC
ACCAAGAAATGTTTCTGTTCTTTGTTTAGACTTGGATTATCACTT    675

                  -10
ysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrG
GCATTTATCTTCAACTGCTCCTATTTAATCCTCTCGTCAAAACTC    720

 1                                 10
lnGluIleCysArgAsnProValThrAspAsnValLysAspIleT
AGGAGATCTGCAGGAATCCTGTGACTGATAATGTAAAAGACATTA    765

     18
hrLysLeu
```

FIG.14B CONT.'

```
CAAAACTGGTAAGTAAAGAATGATTTTGGCATCTATAAGTCTTCC    810

CTGTGCTTGCTGACCACATAGGTTCAGGGCACTCCCGACAGGAGT    855

TCCCAGCTTTCTAAGATAAGGAATCACTGTACGAGTCTGAAGTGC    900

TTCTTCTGGGCAAATGGGAGATGCTTAGGTCATGGAGGGTTTATC    945

TGTATAACTGGCCCTTTGCACACCAACAAAGTGACTGACTGGCTT    990

TTGCCTGTTACCTACTG                               1007

    Intervening sequence of unknown length

TCTCCAGTCCTGGGCATGGTATATACTTAGGCACCCAAGATTGGA     45

TTTACAACTCAAGCATTATATATTGGACAACnACGGGGTATGAGA     90

TATTAATGATATGTCAGGTTGGATGGATGAGTTTTCTCAAGAAAT    135

                                            19
                                           Val
TCTCTTGTATTTACTCACGTTTTCATTTCTTGGTCTCTGTAGGTG    180

                             30
AlaAsnLeuProAsnAspTyrMetIleThrLeuAsnTyrValAla
GCGAATCTTCCAAATGACTATATGATAACCCTCAACTATGTCGCC    225

              39
GlyMetAspValLeu
GGGATGGATGTTTTGGTATGTAGTCCACACACTTCTGAGTTGCCT    270

TTTAGTAGCTAATGGGTGACCTGTGCTTATTCACATTGAAGACAT    315

TATTTGCTCTTTGTCGTTTTTAGATGTTGACCTATAATTTTTCCT    360

TCAAGCTGCTGCTAAGATTATCAGTGAGCATTTCAGTATGTGTTT    405

TAAGCCTACTCATTAAAAGGAAATGGCTCATCTTAGACGTAGCAA    450
```

FIG.14B CONT.'

```
CCGATGTTAATTTTTCCCCAGGCATCTCTCAGAGGGACTTGAATG   495

TTAAAATCATGTTAAATTTCCTCCTTGGCTATGTTATTTCTCATG   540

GCTATGTTATTCCTATTCGTATTTCATTTAAAGGGACGGAATATT   585

TATTGTATTTCTGAACTTTTTCAGGCATGCATCCGGGTCTTTGAA   630

TAAAA                                           635

    Intervening sequence of unknown length

CACTAAGACTCCTTCTAGTAATGTTTGTAATCCTGTCTGTATCGA   45

ATGTCTTTGAAAACGCAGTGACTAAGCCATAAATAATCTTCCACA   90

GAACGTCCAGTGGTTCATGAACTTTGTATGTGGGGGTGGGGCAAG   135

AATTGTCTCACTATTGGTCAAGGAAGAGAAGGTAAGGTATGCAAG   180

GGTGGTTTAATCTTCTTCCGTGGAAGGACAAAATCATCTATCATT   225

TCCTCTGATCTCTATGCATTTGTTTGTTTTGAACTGAATCTGACT   270

TGAGCAAGAGTTGGCGTCCTGTGTTCTGAGGAAACTCTTTGTCCT   315

GCAGTCAGTGACTAAAAGTGCTGAGAGATCTGAAGAGCACTCTGA   360

ATCTGCCATATTTTTAATAGATGCTTTGTCTTCTCTTTGAATTTC   405

     40.                               50
     ProSerHisCysTrpLeuArgAspMetValThrHisLeu
TTCCAGCCTAGTCATTGTTGGTTACGAGATATGGTAACACACTTA   450

                     60
SerValSerLeuThrThrLeuLeuAspLysPheSerAsnIleSer
TCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTTCT   495

     70                                80
GluGlyLeuSerAsnTyrSerIleIleAspLysLeuGlyLysIle
```

FIG.14B CONT.'

GAAGGCTTGAGTAATTATTCCATCATAGACAAACTTGGGAAAATA 540

90 96
ValAspAspLeuValAlaCysMetGluGluAsnAlaProLys
GTGGATGACCTCGTGGCATGTATGGAAGAAAATGCACCTAAGGTA 585

ACTTGGTATTCATCAGAATTATTTTTCTTATACT 619

Intervening sequence of unknown length

GAGCTCATGATGAGCAATTCACAACCACTTGTAATTCCAGCTCCA 45

GAGGACATTATCCCCTCTTTGGATGCCATAGGAATCTGCTCTCAA 90

ATATGTAGATACCACCTCTGCCACCTCAGCACATACATACACATA 135

ATTAAAAAATAGAAACATTAAAGGAGTTCCAATCAATCCTTATTC 180

TTTTCTGTATTCAGTATGCCCAGATGTAAATTCTAGGAATATGTT 225

TTAAAGGCTAATTCTTATTTTGTAATAAGCAGCTTTAAAATTCTT 270

AATTGTTTTTTCGGGTCACTTTATTGTCCTATTGCCACGACATTG 315

TCCTGTCCCATTGTCTGTTATTCCTTCTGTTTTGTTTATTGTTCC 360

CTAGTTACTTTGATCATGAGATTGACCTGTTACCCGTTGTTATTC 405

TCTGTAGCCATTTTGAGTTGTGTCTATTAGAACAGCTGTTAAATT 450

ACTTGAATCATTGAGGACATAGTCAATAATCTATTATGCTGATCC 495

AGTCAAGTCTATGAGTTATTTGAAAACTAGAATCTTTGTTAATTA 540

97
AsnValLys
TTTGTTTGCTTGTTTGTTTGTTTATTATTTGTCTAGAATGTAAAA 585

100 110
GluSerLeuLysLysProGluThrArgAsnPheThrProGluGlu

FIG.14B CONT.'

GAATCACTGAAGAAGCCAGAAACTAGAAACTTTACTCCTGAAGAA 630

120
PhePheSerIlePheAsnArgSerIleAspAlaPheLysAspPhe
TTCTTTAGTATTTTCAATAGATCCATTGATGCCTTCAAGGACTTC 675

130 140
MetValAlaSerAspThrSerAspCysValLeuSerSerThrLeu
ATGGTGGCATCTGACACTAGTGATTGTGTGCTCTCTTCAACATTA 720

148
GlyProGluLysA
GGTCCTGAGAAAGGTAAGGCTTTTAAGCATTTCTTGTTTAAATGT 765

ACATAGAAAGCCTGAACTTCTGTAAGCCTCTACTGCTGAATCAAC 810

TAAATGTGTTGCTGTAGAAAGAACGTGTGGGTTTTTCTGATAAAA 855

ACAAAAAGCAAATATCAATGACTACCAATGATTATTATCTAGCTT 900

GAGAGATATGCCCTAAGACAGCGATTCTCGATATTTCTAAATTAA 945

AGAATTGTGTGATGGTGGCTCACATATTTTCTAACTGTGATATTT 990

GCCAGGAGAGTAGAATAATGTTATTCTTCATCCCCAGAATTCCTA 1035

AGATTTCACGTCTCATGTCTTTTCCATAAGGTTCAAACTCTGAGA 1080

CTTGAGTTCTGAGCCTCAGCAGGTCATTCTGAATCCCCACTCTCC 1125

CCGAGCTGGGTCCCTATGGGGAACTAACTTCATTGCTTTCTTTT 1170

AAAACATGACGAGTTACCAACAGCTCCTCGCTATTATAAACATGT 1215

TCCTAAGCATGTCTGTGCATGCaATAAGCCTTCACTCTACAAGAC 1260

AGTTATGGTGTATCGCTTGACAAAACTGAGCAGCCAAGCTGAGTA 1305

TGAAATAATAATCTAGACTTGGGAGGCAGACCCAGCACCTACTGT 1350

GATATTGCACTTCGCCTTTGGGGACTCTATGATTCAAAAGTTCA 1395

FIG.14B CONT.

```
                                                    150
                                                spSerArgV
CCATGTAACACTGACACATTATTGCTTTCTATTTAGATTCCAGAG   1440

                        160
alSerValThrLysProPheMetLeuProProValAlaAlaSerS
TCAGTGTCACAAAACCATTTATGTTACCCCCTGTtGCAGCCAGTT   1485

     170                    176
erLeuArgAsnAspSerSerSerSerAsn_
CCCTTAGGAATGACAGCAGTAGCAGTAATAGTAAGTACACATATC   1530

TGATTTACTGCATGCATGGCTCCAAGTATCCTCTATAGGAGTGTT   1575

GCATGGACTTAAAGTTTATAAATCACTACTAATAATGCTGTTCTG   1620

TCACTGTTATTCCTTGTATGGGCTTCCTGACAATTAAATATCTGG   1665

TTTGTAGAATCGGATCTCCTTAGAGGTTAAGATGACCATGACAAA   1710

ATTAGGCCAATCAACTTTCTGCGAAGGTTATTTAAATAAGGCAC   1755

GAAATTAATTGAAGGAAAAAAAAATACAAGCAAGGCCTTATTTTG   1800

AATCATGGTAGGCTTAAAATAGACTTTGTGGAGAATGTCCCTGAT   1845

CAAAGTGGAGTTTTCAGATTTCAAGTGCATGTGCTAACTCTCCAC   1890

AATGTCAAGGCTATTTTCAGTTTTGTGTCTCCATATTTACTACTG   1935

CATGTTTGGAAATTTGCTGATGCTGTTAGATTACCTAAGAATGTA   1980

TGTTGAAGAAGAATGGACTTCTTTCCCTAAAATTTCTGTCCTCTT   2025

TGcCCAAGAACCCAcGTTCCTGGAAGACTATCTTATTTTCATGTC   2070

TGTGCAATGATCATTATAAAGATTATTGAATATACTGGGAATACT   2115

CTGGTTTCTGTTTTTACAGATTCATAATAGCTTATTCAGTCTTTA   2160

AAGAAAGTTCTCTGAAGTCCATGCTTTAGAATGTTTCTCTATCAA   2205
```

FIG.14B CONT.'

AACTTGACCTGGACCTTAAATAAAGCTATATTTAGTCTTTTTATC 2250

CCTGAAAAATATATTTCACAGTGTAGACATTTGATATACATCTAA 2295

GGGAAGGATGCTGCCAGAATGCTCGGGCTGGCAGTCTACAAAGTC 2340

CACTGCTCTCAGGATGGACTTCTGAAAGCGGAAATTGTGAACTGC 2385

ATGCATATAACATATCAGATCCTCGAGC 2413

FIG.14C

```
                                   -25          -20
                                    M  K  K  T  Q  T  W  I  I  T  C  I
CTGGATCGCAGCGCTGCCTTTCCTTATGAAGAAGACACAAACTTGGATTATCACTTGCAT   60

         -10                    1
 Y  L  Q  L  L  L  F  N  P  L  V  K  T  Q  E  I  C  R  N  P
TTATCTTCAACTGCTCCTATTTAATCCTCTCGTCAAAACTCAGGAGATCTGCAGGAATCC  120

      10                            20
 V  T  D  N  V  K  D  I  T  K  L  V  A  N  L  P  N  D  Y  M
TGTGACTGATAATGTAAAAGACATTACAAAACTGGTGGCGAATCTTCCAAATGACTATAT  180

      30                            40
 I  T  L  N  Y  V  A  G  M  D  V  L  P  S  H  C  W  L  R  D
GATAACCCTCAACTATGTCGCCGGGATGGATGTTTTGCCTAGTCATTGTTGGTTACGAGA  240

      50                            60
 M  V  T  H  L  S  V  S  L  T  T  L  L  D  K  F  S  N  I  S
TATGGTAACACACTTATCAGTCAGCTTGACTACTCTTCTGGACAAGTTTTCAAATATTTC  300

      70                            80
 E  G  L  S  N  Y  S  I  I  D  K  L  G  K  I  V  D  D  L  V
TGAAGGCTTGAGTAATTATTCCATCATAGACAAACTTGGGAAAATAGTGGATGACCTCGT  360

      90                            100
 A  C  M  E  E  N  A  P  K  N  V  K  E  S  L  K  K  P  E  T
GGCATGTATGGAAGAAAATGCACCTAAGAATGTAAAAGAATCACTGAAGAAGCCAGAAAC  420

      110                           120
 R  N  F  T  P  E  E  F  F  S  I  F  N  R  S  I  D  A  F  K
TAGAAACTTTACTCCTGAAGAATTCTTTAGTATTTTCAATAGATCCATTGATGCCTTCAA  480
```

FIG.14C CONT.'

```
        130                                140
 D  F  M  V  A  S  D  T  S  D  C  V  L  S  S  T  L  G  P  E
GGACTTCATGGTGGCATCTGACACTAGTGATTGTGTGCTCTCTTCAACATTAGGTCCTGA   540

        150                                160
 K  D  S  R  V  S  V  T  K  P  F  M  L  P  P  V  A  A  S  S
GAAAGATTCCAGAGTCAGTGTCACAAAACCATTTATGTTACCCCCTGTTGCAGCCAGTTC   600

        170                                180
 L  R  N  D  S  S  S  S  N  R  K  A  A  K  S  P  E  D  P  G
CCTTAGGAATGACAGCAGTAGCAGTAATAGGAAAGCCGCAAAGTCCCCTGAAGACCCAGG   660

        190                                200
 L  Q  W  T  A  M  A  L  P  A  L  I  S  L  V  I  G  F  A  F
CCTACAATGGACAGCAATGGCACTGCCGGCTCTCATTTCGCTTGTAATTGGCTTTGCTTT   720

        210                                220
 G  A  L  Y  W  K  K  K  Q  S  S  L  T  R  A  V  E  N  I  Q
TGGAGCCTTATACTGGAAGAAGAAACAGTCAAGTCTTACAAGGGCAGTTGAAAATATACA   780

        230                                240
 I  N  E  E  D  N  E  I  S  M  L  Q  Q  K  E  R  E  F  Q  E
GATTAATGAAGAGGATAATGAGATAAGTATGTTGCAACAGAAAGAGAGAGAGTTTCAAGA   840

248
 V
GGTGTAATT                                                      849
```

FIG.15A

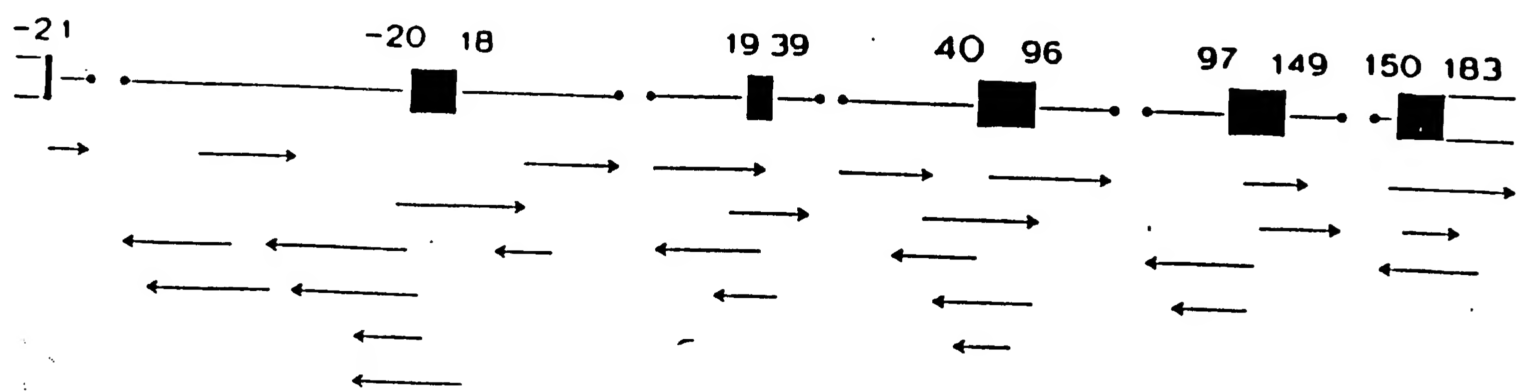


FIG.15B

-21
hrGln

CACAAGTGAGTAGGGCGCGCCCGGGAGCTCCCAGGCTCTCCAGGA 45

AAAATCGCGCCCGGTGCCCCGGGGaAGCCGGCGCTCCCTGGGACT 90

TGCAGCTGGGGCGTGCAGGGCTGTGCCTGCCGGGTG 126

Intervening sequence of unknown length

AGATACTACAAAGATAAATCAGTTGCACAAGTTCTTGAAACTCTA 45

CAGTGTAATAAGGAAAAATAAGTCATGCATAAAAGCAACTATAAT 90

ACATAATAGAAAATGTTATTTTCAAGCCGATGTGTAGGTTATGTG 135

TGTTCGAGAGAGAGAGAGAGAAGACAGATTACTTTCTGCTAGGGT 180

TCAAGAATGCCTTCCTGTTGGCTAAGGAAATATTTTCCTTAAGTG 225

GCTAAAAAGCTGTGTTTCAAAATATTCTTTTGATGTCTCACAAAT 270

TCAGTGGAATTCTCTTAGGTCTAAAAATATACATCTCTCTCACTT 315

TAACTTGGTGTGCTATTGTAGATTATTGGATTAAAGCACTGCTCA 360

GGGATTATGCTGCTTCTTGCCAAGCAGTCTACATTTAAAGTAGAA 405

ATAAGATGTTTCTTTTGGTGCCATAAGGTATACATTTTATGCATT 450

CTCTAGTTTTTAGAAGATACCCTAAGGGCTAAGTCTTTAACATGC 495

TGCTACAAGTTTATTCCTAATTGCCATTGGGAAATTGGCTGAAGA 540

AAGTTTTTAACAAAAGTTAACAATATTGTCATTGAGAGAATAATT 585

CAAAATGGATTTTAACTAAAAGCTTTTAAAAACTTTGGTGAGCAT 630

AGCTTGAATGCGTAATATTTAATTGCATTTAAGCCAATAACATAT 675

FIG.15B CONT.'

```
ATTAGACTGGTCTTTTTGTGCATCAAGGCATTAGATGTTAAAAGT     720

TTGAATGATTACAGATCTTAACTGATGATCACCAAGCAATTTTTC     765

                  -20                                  -10
                  ThrTrpIleLeuThrCysIleTyrLeuGlnLe
TGTTTTCATTTAGACTTGGATTCTCACTTGCATTTATCTTCAGCT     810

                                              1
uLeuLeuPheAsnProLeuValLysThrGluGlyIleCysArgAs
GCTCCTATTTAATCCTCTCGTCAAAACTGAAGGGATCTGCAGGAA     855

            10                                18
nArgValThrAsnAsnValLysAspValThrLysLeu
TCGTGTGACTAATAATGTAAAAGACGTCACTAAATTGGTAAGTAA     900

GGAATGCTTTACCGTGCTGTGTAAAAAAGAGCTGTGGCTCTTTTT     945

CCTGTGCTTGTTGATAAAAGATTTAGATTTTTCTTGCCCCAAAGT     990

AATGTTTTCCTAAAGTGGGGAAAGTAATCACTGGGTTACAATAAA     1035

GGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA     1080

TTTGTTGGTAAAACTGGCTAGTTGCACACCACTGCTGTGACTGCT     1125

TCTTTGCTGGTCTTCTCCCCATCCTTCATAGGCAGTGAAGGACCT     1170

TGGAGAGTTCGCTGTGTGCTGATGGGCTTGCCCCAGCTTGTTCCC     1215

CATAATCTCTCCAGTGGGTTTCCCAGCATGTTCTATTCCCCTTCA     1260

CATGTCTTCCTACTCTTCTTTAAAAAGCCTAACGAAAGGAAATCT     1305

GAAATGGCTATTCTCCCAATTCAATCAGCAGGAAGACCCTGTCAC     1350

ATGTCAGTGGGTGTTTGCTCCTTCAGGGAACATAGAGAGGTGATT     1395

CATTGCCCACATGTTGAAGGGACTCATCTCCCTGGTTTGTCACAT     1440

TGAACTCTTCCCTCAGCGAAAGCATTTGCATTGCTTCCC           1479
```

FIG.15B CONT.'

Intervening sequence of unknown length

```
GAATTCCAAGATCACAGGTGGAAGCTGAAATTCAGATCATGTTTC    45

CAAAACTCAGTAGGTTATACCTAGCCAGGCATAACTGAATTTGGA    90

GTCTAAAAGATCTGTATTATCACTTTTTTATTTTGAAGGATGCCT   135

TTTGATTACAGAGGGAAATCAAGGATTAAAAATCAATATACATGT   180

AAATATTGAAATTCATTGGTAACTTTAAAAAGCACAACAGTTTTG   225

TGTGCTTTTCTCCAAAGCACTACAAATATGATTAATTGATGTATA   270

                                         19
                                       ValAlaA
AGAATTTTCTTATGGAATTTTTTTTTTTGTCTCTGTAGGTGGCAA   315

                              30
snLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM
ATCTTCCAAAAGACTACATGATAACCCTCAAATATGTCCCCGGGA   360

          39
etAspValLeu
TGGATGTTTTGGTATGTAAACTACATTTCTGAGTTTCATTTTAGT   405

AGCTCATAGAAGAAATGGGATCATTCATATTGAGATAGTACACTA   450

GCTGCTATTTAGGAGCTTGCTTATTGTCAGGATTTGAAGAATTTA   495

TCTTTGGAATTTGACTTGCAGGCTTTTTTTTCCCCCTCTT   535
```

Intervening sequence of unknown length

```
CCTGTTACAAGAGTCCCTCCTCCTATTACAATAGTCCCTCCTCCT    45

CCTGTCACACTAGTCCCTTCTCTTCCTGTTACAATAACCCCTGTC    90
```

FIG.15B CONT.'

CTCCTATTACAACATTTTAAGTAATGTAATATTAATTTTAAAAAT 135

CTGGCCAGGCACGGTGGTTCATGCTTGTAATCCCAGCACATTGGG 180

AAGCTGAGACGGGTGGATCATTTGAGGTCAGGAAGTTTGAGACAG 225

CCTGGCCAACATGGTGAAACTTCCTCTCTACTAAAAATAAAAAAG 270

TAGCCAGGCATGGTGGCAGGCACTTGTAATCTGAGCTACTCGAGA 315

GGCTGAGGCAGGAGAATCACTTGAGTAACTAAAACGATAGCTTTG 360

AAGAGTACTCCGAGTTTTATGGCACTTACTTATTAAAATAGCTGT 405

40
ProSerHisCysTrpIleS
TTTGTCTCTTTTTTCATATCTTGCAGCCAAGTCATTGTTGGATAA 450

50 60
erGluMetValValGlnLeuSerAspSerLeuThrAspLeuLeuA
GCGAGATGGTAGTACAATTGTCAGACAGCTTGACTGATCTTCTGG 495

70
spLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI
ACAAGTTTTCAAATATTTCTGAAGGCTTGAGTAATTATTCCATCA 540

80 90
leAspLysLeuValAsnIleValAspAspLeuValGluCysValL
TAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTGA 585

96
ysGluAsnSerSerLys
AAGAAAACTCATCTAAGGTAACTTTGTGTTCATTGGGATTATTTT 630

TCATTACGCTTCTCTAAAAACCCATGCTTCTTGGTGCTGTTGGGG 675

AAAATGAGGCACCTTTATTTATGATATTTTGATTGTATAAACTTC 720

AAATTTAAAAATCTTGTTCAGATGAGCAAAGAAAACAAGTATTTG 765

CAGTTATACTGCAATACTGAAGTGCACATTC 796

FIG.15B CONT.'

Intervening sequence of unknown length

```
TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCACTGGGATCA    45

CTACCCTGCATTACCAATCTGAATTACATACGTTAAAACAGCCAT    90

CTAAAAGTGCTAGTTGTAAGAGTCTAAATACTTGAATCTTTGAGA   135

GACATATTTATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA   180

                                         97
                                       AspLeuLysL
CTATTTGAAAAATGTAATCCTATTTTTTCTTCTAGGATCTAAAAA   225

                            110
ysSerPheLysSerProGluProArgLeuPheThrProGluGluP
AATCATTCAAGAGCCCAGAACCCAGGCTCTTTACTCCTGAAGAAT   270

                 120                           130
hePheArgIlePheAsnArgSerIleAspAlaPheLysAspPheV
TCTTTAGAATTTTTAATAGATCCATTGATGCCTTCAAGGACTTTG   315

                                 140
alValAlaSerGluThrSerAspCysValValSerSerThrLeuS
TAGTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAA   360

      148
erProGluLysA
GTCCTGAGAAAGGTAAGACATGTAAGCATTTCCAGTTCAAATGTA   405

AACAACAAACTTAAATCTTCCCTATGTAGTAAGAATCTACCTCTG   450

TGTTAAGCTGTAGCAAGATACATGCATGTACGTCTAATAAAAAAG   495

CAGATATCAATAGCACAGAAGAAA                        519
```

Intervening sequence of unknown length

FIG.15B CONT.'

```
CTCTATAACTCATACAAATCACCATATAACACTGACACATTATTG      45

                150                                  160
             spSerArgValSerValThrLysProPheMetL
CTTTCTATTTAGATTCCAGAGTCAGTGTCACAAAACCATTTATGT      90

                             170
euProProValAlaAlaSerSerLeuArgAsnAspSerSerSerS
TACCCCCTGTTGCAGCCAGCTCCCTTAGGAATGACAGCAGTAGCA     135

  176
erAsnA
GTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCA     180

ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCT     225

ACATTTATTATTATTGATACTGTTCTGTTACTGTTATTCCTTTTA     270

TGGTCTTCTTGAGACTTAAGTTTGTAGAATTAAATTTCCCTAGAG     315

CTGGAGATAATGTTTAGAGAATTAGGCCAATAAATTT             352
```

FIG.15C

```
                  -25            -20
                   M  K  K  T  Q  T  W  I  L  T  C  I  Y  L  Q
AAGCTTGCCTTTCCTTATGAAGAAGACACAAACTTGGATTCTCACTTGCATTTATCTTCAG   61

-10                               1                          10
 L  L  L  F  N  P  L  V  K  T  E  G  I  C  R  N  R  V  T  N
CTGCTCCTATTTAATCCTCTCGTCAAAACTGAAGGGATCTGCAGGAATCGTGTGACTAAT  121

                           20                            30
 N  V  K  D  V  T  K  L  V  A  N  L  P  K  D  Y  M  I  T  L
AATGTAAAAGACGTCACTAAATTGGTGGCAAATCTTCCAAAAGACTACATGATAACCCTC  181

                           40                            50
 K  Y  V  P  G  M  D  V  L  P  S  H  C  W  I  S  E  M  V  V
AAATATGTCCCCGGGATGGATGTTTTGCCAAGTCATTGTTGGATAAGCGAGATGGTAGTA  241

                           60                            70
 Q  L  S  D  S  L  T  D  L  L  D  K  F  S  N  I  S  E  G  L
CAATTGTCAGACAGCTTGACTGATCTTCTGGACAAGTTTTCAAATATTTCTGAAGGCTTG  301

                           80                            90
 S  N  Y  S  I  I  D  K  L  V  N  I  V  D  D  L  V  E  C  V
AGTAATTATTCCATCATAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTG  361

                          100                           110
 K  E  N  S  S  K  D  L  K  K  S  F  K  S  P  E  P  R  L  F
AAAGAAAACTCATCTAAGGATCTAAAAAAATCATTCAAGAGCCCAGAACCCAGGCTCTTT  421
```

FIG.15C CONT.'

```
                                120                                 130
 T   P   E   E   F   F   R   I   F   N   R   S   I   D   A   F   K   D   F   V
ACTCCTGAAGAATTCTTTAGAATTTTTAATAGATCCATTGATGCCTTCAAGGACTTTGTA    481

                                140                                 150
 V   A   S   E   T   S   D   C   V   V   S   S   T   L   S   P   E   K   D   S
GTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAAGTCCTGAGAAAGATTCC    541

                                160                                 170
 R   V   S   V   T   K   P   F   M   L   P   P   V   A   A   S   S   L   R   N
AGAGTCAGTGTCACAAAACCATTTATGTTACCCCCTGTTGCAGCCAGCTCCCTTAGGAAT    601

                                180         183
 D   S   S   S   S   N   S   K   Y   I   Y   L   I
GACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCAAT    661

TAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCTACATTTATTATTATTGA    721

TACTGTTCTGTTACTGTTATTCCTTTTATGGTCTTCTTGAGACTTAAGTTTGTAGAATTA    781

AATTTCCCTAGAGCTGGAGATAATGTTTAGAGAATTAGG                         820
```

FIG. 15D

```
GAGCTCCGAGCcCTCtCTGGCGCgCgAGGTATTTCGTCTGTnCCCGGGGGTGCCAGGTGA   60
GCCCCAGCGGATCCGGGAGGGTAAGCTGGGACTCCTCGCGAGCAGTAGCTGCAGGGTACC  120
AAGCTTCGCCCTCTGCGTCCCCGCGCCTTCGCGGTCTCCCGCCAGTGCAGGTCCGGGGCC  180
CCCAGGCGAGCGGACAAGGTTGGCCTAATCTGCCAAACTTCTGGGGCATTTACCGTGCTC  240
TGGCCGCCCTCCCGATTCTTCCCTCCGCGCCCTTGCCTGCTTCTCGCCTACCCCGGGCTC  300
CGGAAGGGAAGGAGGCGTGTCCGGAGCAGGCGGGCGGGAACTGTATAAAAGCGCCGGCGG  360
CTCAGCAGCCGGCTTCGCTCGCCGCCTCGCGCCGAGACTAGAAGCGCTGCGGGAAGCAGG  420
GACAGTGGAGAGGGCGCTGCGCTCGGGCTACCCAATGCGTGGACTATCTGCCGCCGCTGT  480
TCGTGCAATCACCCTGGAGCTCCAGAACAGCTAAACGGAGTCGCCACACCACTGTTTGTGC  540

                                       -25         -21
                                       MetLysLysThrGln
TGGATCGCAGGGCTGCCTTTCCTTATGAAGAAGACACAAGTGAGTAGGGCGCGCCCGGGA  600
GCTCCCAGGCTCTCCAGGAAAAATCGCGCCCGGTGCCCCGGGGAAGCCGGCGCTCCCTGG  660
GACTTGCAGCTGGGGCGTGCAGGGCTGTGCCTGCCGGGTGAGACAAGAGGATGCGGGGGA  720
GGCCGGCGTGGTGTGTGATCCCGAGCCGAGCCGnnTGAGCCAGGGAGAAAAGGAGTGGGA  780
GTnCTGAGAGGGAGCCAGTGTCAAGTTTGGAGCCTCAGCAGTTAAGTTTTGAGCTGTCAG  840
TCGGAAACCGTAATTCCCGTCTGGTGGAAAGATTGGCTTTTnGnCCACGGAATGTAAGTT  900
ATCAC                                                         905
```

FIG. 15D CONT.

Intervening sequence of unknown length

```
AGATACTACAAAGATAAATCAGTTGCACAAGTTCTTGAAACTCTACAGTGTAATAAGGAA    60

AAATAAGTCATGCATAAAAGCAACTATAATACATAATAGAAAATGTTATTTTCAAGCCGA   120

TGTGTAGGTTATGTGTGTTCGAGAGAGAGAGAGAGAAGACAGATTACTTTCTGCTAGGGT   180

TCAAGAATGCCTTCCTGTTGGCTAAGGAAATATTTTCCTTAAGTGGCTAAAAAGCTGTGT   240

TTCAAAATATTCTTTTGATGTCTCACAAATTCAGTGGAATTCTCTTAGGTCTAAAAATAT   300

ACATCTCTCTCACTTTAACTTGGTGTGCTATTGTAGATTATTGGATTAAAGCACTGCTCA   360

GGGATTATGCTGCTTCTTGCCAAGCAGTCTACATTTAAAGTAGAAATAAGATGTTTCTTT   420

TGGTGCCATAAGGTATACATTTTATGCATTCTCTAGTTTTTAGAAGATACCCTAAGGGCT   480

AAGTCTTTAACATGCTGCTACAAGTTTATTCCTAATTGCCATTGGGAAATTGGCTGAAGA   540

AAGTTTTTAACAAAAGTTAACAATATTGTCATTGAGAGAATAATTCAAAATGGATTTTAA   600

CTAAAAGCTTTTAAAAACTTTGGTGAGCATAGCTTGAATGCGTAATATTTAATTGCATTT   660

AAGCCAATAACATATATTAGACTGGTCTTTTTGTGCATCAAGGCATTAGATGTTAAAAGT   720

                                                          -20
                                                           Th
TTGAATGATTACAGATCTTAACTGATGATCACCAAGCAATTTTTCTGTTTTCATTTAGAC   780

                  -10
rTrpIleLeuThrCysIleTyrLeuGlnLeuLeuLeuPheAsnProLeuValLysThrGl
TTGGATTCTCACTTGCATTTATCTTCAGCTGCTCCTATTTAATCCTCTCGTCAAAACTGA   840
```

```
1                                       10                                  18
uGlyIleCysArgAsnArgValThrAsnAsnValLysAspValThrLysLeu
AGGGATCTGCAGGAATCGTGTGACTAATAATGTAAAAGACGTCACTAAATTGGTAAGTAA    900

GGAATGCTTTACCGTGCTGTGTAAAAAAGAGCTGTGGCTCTTTTTCCTGTGCTTGTTGAT    960

AAAAGATTTAGATTTTTCTTGCCCCAAAGTAATGTTTTCCTAAAGTGGGGAAAGTAATCA    1020

CTGGGTTACAATAAAGGGTTTATAGAAAGCAGGTAGTGAGATATTTAGGGTCATGGATAA    1080

TTTGTTGGTAAAACTGGCTAGTTGCACACCACTGCTGTGACTGCTTCTTTGCTGGTCTTC    1140

TCCCCATCCTTCATAGGCAGTGAAGGACCTTGGAGAGTTCGCTGTGTGCTGATGGGCTTG    1200

CCCCAGCTTGTTCCCCATAATCTCTCCAGTGGGTTTCCCAGCATGTTCTATTCCCCTTCA    1260

CATGTCTTCCTACTCTTCTTTAAAAAGCCTAACGAAAGGAAATCTGAAATGGCTATTCTC    1320

CCAATTCAATCAGCAGGAAGACCCTGTCACATGTCAGTGGGTGTTTGCTCCTTCAGGGAA    1380

CATAGAGAGCTGATTCATTGCCCACATGTTGAAGGGACTCATCTCCCTGGTTTGTCACAT    1440

TGAACTCTTCCCTCAGCGAAAGCATTTGCATTGCTTCCC                         1479


               Intervening sequence of unknown length


GAATTCCAAGATCACAGGTGGAAGGTGAAATTCAGATCATGTTTCCAAAACTCAGTAGGT    60

TATACCTAGCCAGGCATAACTGAATTTGGAGTCTAAAAGATCTGTATTATCACTTTTTTA    120

TTTTGAAGGATGCCTTTTGATTACAGAGGGAAATCAAGGATTAAAAATCAATATACATGT    180
```

FIG. 15D CONT.

```
AAATATTGAAATTCATTGGTAACTTTAAAAAGCACAACAGTTTTGTGTGCTTTTCTCCAA    240

AGCACTACAAATATGATTAATTGATGTATAAGAATTTTCTTATGGAATTTTTTTTTTTGT    300

        19                                      30
        ValAlaAsnLeuProLysAspTyrMetIleThrLeuLysTyrValProGlyM
CTCTGTAGGTGGCAAATCTTCCAAAAGACTACATGATAACCCTCAAATATGTCCCCGGGA    360

        39
etAspValLeu
TGGATGTTTTGGTATGTAAACTACATTTCTGAGTTTCATTTTAGTAGCTCATAGAAGAAA    420

TGGGATCATTCATATTGAGATAGTACACTAGCTGCTATTTAGGAGCTTGCTTATTGTCAG    480

GATTTGAAGAATTTATCTTTGGAATTTGACTTGCAGGCTTTTTTTTCCCCCTCTT         535

                  Intervening sequence of unknown length

CCTGTTACAAGAGTCCCTCCTCCTATTACAATAGTCCCTCCTCCTCCTGTCACACTAGTC    60

CCTTCTCTTCCTGTTACAATAACCCCTGTCCTCCTATTACAACATTTTAAGTAATGTAAT    120

ATTAATTTTAAAAATCTGGCCAGGCACGGTGGTTCATGCTTGTAATCCCAGCACATTGGG    180

AAGCTGAGACGGGTGGATCATTTGAGGTCAGGAAGTTTGAGACAGCCTGGCCAACATGGT    240

GAAACTTCCTCTCTACTAAAAATAAAAAAGTAGCCAGGCATGGTGGCAGGCACTTGTAAT    300

CTGAGCTACTCGAGAGGCTGAGGCAGGAGAATCACTTGAGTAACTAAAACGATAGCTTTG    360

AAGAGTACTCCGAGTTTTATGGCACTTACTTATTAAAATAGCTGTTTTGTCTCTTTTTTC    420
```

FIG. 15D CONT.

```
         40                            50
         ProSerHisCysTrpIleSerGluMetValValGlnLeuSerAspSerL
ATATCTTGCAGCCAAGTCATTGTTGGATAAGCGAGATGGTAGTACAATTGTCAGACAGCT    480

         60                            70
euThrAspLeuLeuAspLysPheSerAsnIleSerGluGlyLeuSerAsnTyrSerIleI
TGACTGATCTTCTGGACAAGTTTTCAAATATTTCTGAAGGCTTGAGTAATTATTCCATCA    540

         80                            90
leAspLysLeuValAsnIleValAspAspLeuValGluCysValLysGluAsnSerSerL
TAGACAAACTTGTGAATATAGTGGATGACCTTGTGGAGTGCGTGAAAGAAAACTCATCTA    600
96
ys
AGGTAACTTTGTGTTCATTGGGATTATTTTTCATTACGCTTCTCTAAAAACCCATGCTTC    660

TTGGTGCTGTTGGGGAAAATGAGGCACCTTTATTTATGATATTTTGATTGTATAAACTTC    720

AAATTTAAAAATCTTGTTCAGATGAGCAAAGAAAACAAGTATTTGCAGTTATACTGCAAT    780

ACTGAAGTGCACATTC                                                796
```

Intervening sequence of unknown length

```
TTGTGTTCACTGCCCCAGATTCAACTTGTGATCCCACTGGGATCACTACCCTGCATTACC    60

AATCTGAATTACATACGTTAAAACAGCCATCTAAAAGTGCTAGTTGTAAGAGTCTAAATA    120

CTTGAATCTTTGAGAGACATATTTATAGTCCATTATCTTCACCTCAGTTAAGTCTGAAGA    180

                                    97
                                   AspLeuLysLysSerPheLysSerP
CTATTTGAAAAATGTAATCCTATTTTTTCTTCTAGGATCTAAAAAAATCATTCAAGAGCC    240
```

FIG. 15D CONT.

```
                110                                 120
roGluProArgLeuPheThrProGluGluPhePheArgIlePheAsnArgSerIleAspA
CAGAACCCAGGCTCTTTACTCCTGAAGAATTCTTTAGAATTTTTAATAGATCCATTGATG    300

                130                                 140
laPheLysAspPheValValAlaSerGluThrSerAspCysValValSerSerThrLeuS
CCTTCAAGGACTTTGTAGTGGCATCTGAAACTAGTGATTGTGTGGTTTCTTCAACATTAA    360

         148
erProGluLysA
GTCCTGAGAAAGGTAAGACATGTAAGCATTTCCAGTTCAAATGTAAACAACAAACTTAAA    420

TCTTCCCTATGTAGTAAGAATCTACCTCTGTGTTAAGCTGTAGCAAGATACATGCATGTA    480

CGTCTAATAAAAAAGCAGATATCAATAGCACAGAAGAAACTAATGATTGTAGATTTGTGGG   541


                Intervening sequence of unknown length


                                                         spS
CTCTATAACTCATACAAATCACCATATAACACTGACACATTATTGCTTTCTATTTAGATT    60

150                          160
erArgValSerValThrLysProPheMetLeuProProValAlaAlaSerSerLeuArgA
CCAGAGTCAGTGTCACAAAACCATTTATGTTACCCCCTGTTGCAGCCAGCTCCCTTAGGA    120

170             176
snAspSerSerSerSerAsnA
ATGACAGCAGTAGCAGTAATAGTAAGTACATATATCTGATTTAATGCATGCATGGCTCCA    180

ATTAGCACCTATAGGAGTATTGCATGGGCTTTCAAGGAAACTTCTACATTTATTATTATT    240

GATACTGTTCTGTTACTGTTATTCCTTTTATGGTCTTCTTGAGACTTAAGTTTGTAGAAT    300
```

FIG. 15D CONT.

FIG. 15D CONT.

```
TAAATTTCCCTAGAGCTGGAGATAATGTTTAGAGAATTAGGCCAATAAATTTTCTGCTGA    360

GGTTATTTTAAATAAGACATAAAATTAATTTTAGAAATATGATTTATGCCTTTTGTTGAA    420

TCATTAACATATAT                                                  434


                  Intervening sequence of unknown length


ACAGAAACAGTTAAAACAACCACAGCATAAGAGnAAAACTTCTAGAATGGATATGCTGTA    60

                              178
                           rgLysAlaLysAsnProProGlyAspSerSerL
TTCATCAGTGTGTTCTTTAAATTATAGGGAAGGCCAAAAATCCCCCTGGAGACTCCAGCC    120

    190                          200
euHisTrpAlaAlaMetAlaLeuProAlaLeuPheSerLeuIleIleGlyPheAlaPheG
TACACTGGGCAGCCATGGCATTGCCAGCATTGTTTTCTCTTATAATTGGCTTTGCTTTTG    180

             213
lyAlaLeuTyrTrpLys
GAGCCTTATACTGGAAGGTAAGTGGTACCATTCCTTtTTTTAAAAATATGCTATGTtTAC    240

ATAAATTATCATCTTTTTTTCCTCAAGAAATGATCCTTtAAGAAAACAGTGAATCTACCT    300

TAGCTTATACTAAACAAAATTTAAATTTTATAAAGTTTCCTGTTTCTCATTATGTCTGGA    360

GACAATCCCTCTAGCTGATAATTCACGCTTAAGAATTAGGAACT                    404


                  Intervening sequence of unknown length
```

```
AAAACTGTTATTGGAGTTATTGCCATAAAAGATAAAAGTGGAGTCCACTTACCTCTTAAA   60
                                                      214
                                                      LysArgG
TATTAGACCATTCATTGATTATTTTACAGTATATGTCTTTCTTCTTTTTCCAGAAGAGAC   120

        220                   230        235
lnProSerLeuThrArgAlaValGluAsnIleGlnIleAsnGluGluAspAsnGluIleS
AGCCAAGTCTTACAAGGCCAGTTGAAAATATACAAATTAATGAAGAGGATAATGAGATAA   180

e
GGTATTTTGTTTTGCTAAATGTGTgCCCAATCAAGCATGACATTGCCATTTCACACACTG   240

TGTACCTGCCCATAATGTCTTTAAGAAGTCCTTCACTCATGACAGTAGCTCCTAACCAGT   300

GAGTCCCAACTCTATCCATGTTTCTGATGTCTCACTCTCTCTTC                   344

              Intervening sequence of unknown length

GTATGTGTATATGCATATACAGAGAAAGAAATGTTTTAACTACTTGGAAAGACTACCTTA   60

AGACAAATGAAGTCTTCCCTCTTCCCTATAGTAATAAGAAGGTAGGCTCCCCCATTCAAT   120

TTTGCAATCTTCTGCTACTATATTTACAGAAAAGCTGCCTTTTACAATGCCGAGATCATG   180

                                                          rM
GTGTACCTCAGAATCTCTGACCAAGAGCAAATAAGCATTTtTTCTTATTGTTTTTCAGTA   240

237                   248
etLeuGlnGluLysGluArgGluPheGlnGluVal
TGTTGCAAGAGaAAGAGAGAGAGTTTCAAGAAGTGTAATTGTGGCTTGTATCAACACTGT   300

TACTTTCGTACATTGGTAAGTTTTTTCTTCTTTCCTTTTTTTTTCTTTTTTTTATTATA   360
```

FIG. 15D CONT.

CTTTAAGTTCTAGGGTACATGTGCACAATGTGCAGGTTTGTTACGTATGTTTACATGTGC 420

CATGTT 426

FIG. 15D CONT.

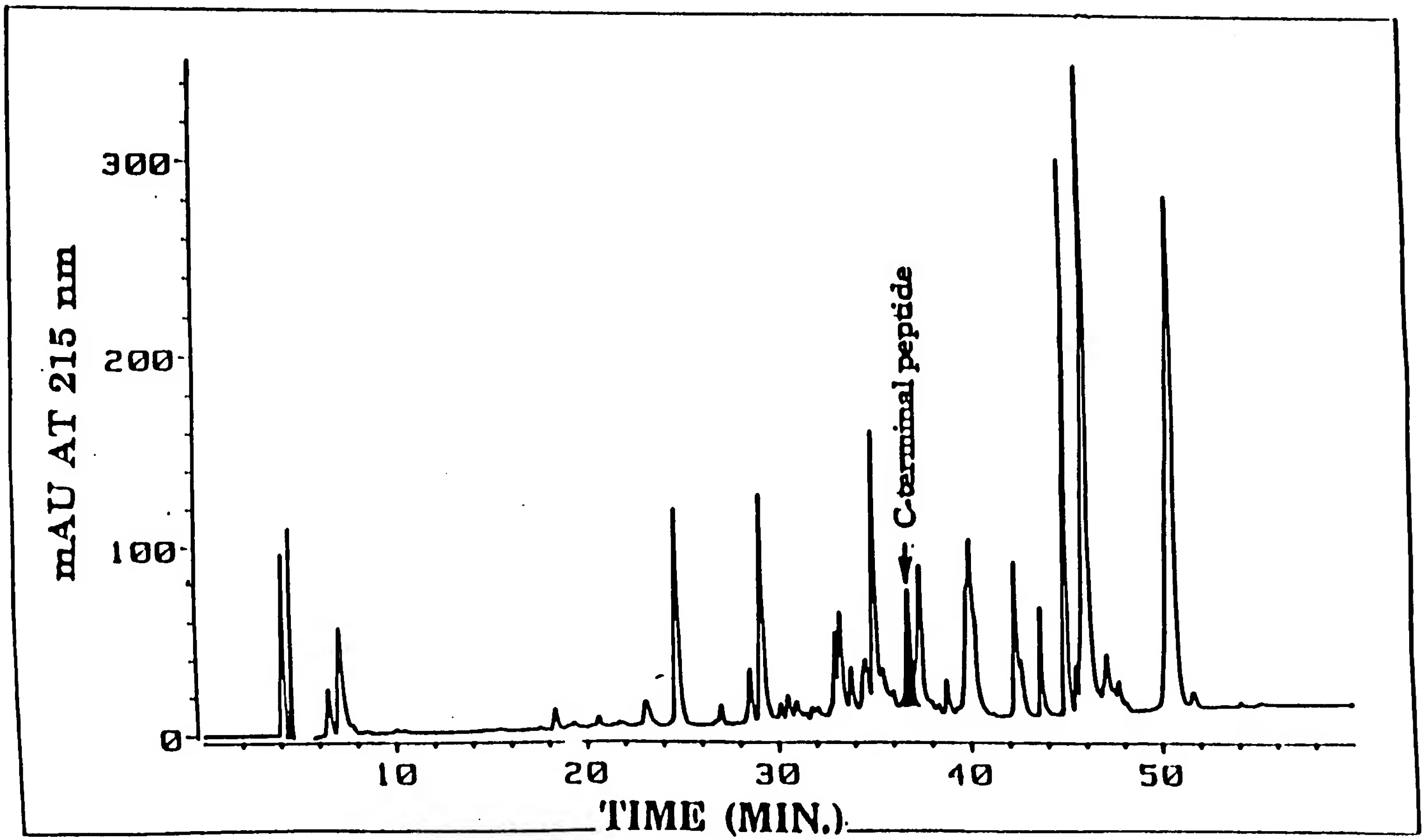
FIG.16A

```
        -25                                                    25
Human    MKKTQTWILT CIYLQLLLFN PLVKTEGICR NRVTNNVKDV TKLVANLPKD
Monkey   MKKTQTWILT CIYLQLLLFN PLVKTEGICR NRVTNNVKDV TKLVANLPKD
Dog      MKKTQTWIIT CIYLQLLLFN PLVKTKGICG KRVTDDVKDV TKLVANLPKD
Cat      MKXTQTWIVT CIYLQXLLFN PLVKTKGLCR NRVTDDVKDV TKLVANLPKD
Cow      MKKTQTWIIT CIYLQLLLFN PLVHTQGICS NRVTDDVKDV TKLVANLPKD
Rat      MKKTQTWIIT CIYLQLLLFN PLVKTQEICR NPVTDNVKDI TKLVANLPND
Mouse    MKKTQTWIIT CIYLQLLLFN PLVKTKEICG NPVTDNVKDI TKLVANLPND
Chicken       TWIIT CFCLQLLLLN PLVKAQSSCG NPVTDDVNDI AKLVGNLPND
Scfpep   MKkTQTWIiT CiyLQlLLfN PLVkt.giCr nrVTd.VkDv tKLVaNLPkD

         26                                                    72
Human    YMITLKYVPG MDVLPSHCWI SEMVVQLSDS LTDLLDKFSN ISEG...LSN
Monkey   YMITLKYVPG MDVLPSHCWI SEMVVQLSDS LTDLLDKFSN ISEG...LSN
Dog      YKIALKYVPG MDVLPSHCWI SVMVEQLSVS LTDLLDKFSN ISEG...LSN
Cat      YKIALKYVPG MDVLPSHCWI SVMVEQLSVS LTDLLDKFSN ISEG...LSN
Cow      YMITLKYVPG MDVLPSHCWI SEMVEQLSVS LTDLLDKFSN ISEG...LSN
Rat      YMITLNYVAG MDVLPSHCWL RDMVTHLSVS LTTLLDKFSN ISEG...LSN
Mouse    YMITLNYVAG MDVLPSHCWL RDMVIQLSLS LTTLLDKFSN ISEG...LSN
Chicken  YLITLKYVPK MDSLPNHCWL HLMVPEFSRS LHNLLQKFSD ISDMSDVLSN
Scfpep   YmItLkYVpg MDvLPsHCWi seMVeqlSvS LtdLLdKFSn ISeg...LSN

         73                                                   121
Human    YSIIDKLVNI VDDLVECVKE NSSKD.LKKS FKSPEPRLFT PEEFFRIFNR
Monkey   YSIIDKLVNI VDDLVECVKE NSSKD.LKKS FKSPEPRLFT PEEFFRIFNR
Dog      YSIIDKLVKI VDDLVECTEG YSFEN.VKKA PKSPELRLFT PEEFFRIFNR
Cat      YSIIDKLVKI VDDLVECVEG HSSEN.VKKS SKSPEPRLFT PEEFFRIFNR
Cow      YCIIDKLVKI VDDLVECMEX HSSEN.VKKS SKSPEPRQFT PEKFFGIFNK
Rat      YSIIDKLGKI VDDLVACMEE NAPKN.VKES LKKPETRNFT PEEFFSIFNR
Mouse    YSIIDKLGKI VDDLVLCMEE NAPKN.IKES PKRPETRSFT PEEFFSIFNR
Chicken  YSIINNLTRI INDLMACLAF DKNKDFIKEN GHLYEEDRFI PENFFRLFNS
Scfpep   YsIIdkLvkI vdDLveC.ee nsskn.vKks .kspEprlFt PEeFFrIFNr
```

FIG.16B

```
         122                                                169
Human    SIDAFKDF.V VASETSDCVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR
Monkey   SIDAFKDF.A VASETSDCVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR
Dog      SIDAFKDLET VASKSSECVV SSTL.SPDKD SRVSVTKPFM LPPVAASSLR
Cat      SIDAFKDLEM VASKTSECVV SSTL.SPEKD SRVSVTKPFM LPPVAASSLR
Cow      SIDAFKDLEI VASKMSECVI SSTS.SPEKD SRVSVTKPFM LPPVAASSLR
Rat      SIDAFKDF.M VASDTSDCVL SSTL.GPEKD SRVSVTKPFM LPPVAASSLR
Mouse    SIDAFKDF.M VASDTSDCVL SSTL.GPEKD SRVSVTKPFM LPPVAASSLR
Chicken  TIEVYKEFAD SLDK.NDCIM PSTVETPEND SRVAVTKTIS FPPVAASSLR
Scfpep   sIdafKdf.m vasktsdCvv sSTl.sPekD SRVsVTKpfm lPPVAASSLR

         170                                                213
Human    NDSSSSNRKA KNPPGD.... ..SSLHWAAM ALPALFSLII GFAFGALYWK
Monkey   NDSSSSNRKA KNPTGD.... ..SSLHWAAM ALPAFFSLII GFAFGALYWK
Dog      NDSSSSNRKA SNSIGD.... ..SNLQWAAM ALPAFFSLVI GFAFGALYWK
Cat      NDSSSSNRKX TNPIED.... ..SSIQWAVM ALPACFSLVI GFAFGAFYWK
Cow      NDSSSSNRKA SNSIED.... ..SSLQWAAV ALPAFFSLVI GFAFGAFYWK
Rat      NDSSSSNRKA AKSPED.... ..PGLQWTAM ALPALISLVI GFAFGALYWK
Mouse    NDSSSSNRKA AKAPED.... ..SGLQWTAM ALPALISLVI GFAFGALYWK
Chicken  NDSIGSNTSS NSNKEALGFI SSSSLQGISI ALTSLLSLLI GFILGAIYWK
Scfpep   NDSssSNrka .n..ed.... ..sslqwaam ALpalfSLvI GFafGAlYWK

         214                                   248
Human    KRQPSLTRAV ENIQIN...E EDNEISMLQE KEREFQEV
Monkey   KRQPSLTRAV ENIQIN...E DDNEISMLQE KEREFQEV
Dog      KKQPNLTRTV ENIQIN...E EDNEISMLQE KEREFQEV
Cat      KKQPNLTRTV ENIQIN...E EDNEISMLQE KEREFQEV
Cow      KKQPNLTRTV ENRQIN...E EDNEISMLQE KEREFQEV
Rat      KKQSSLTRAV ENIQIN...E EDNEISMLQQ KEREFQEV
Mouse    KKQSSLTRAV ENIQIN...E EDNEISMLQQ KEREFQEV
Chicken  KTHPKSRPES NETIQCHGCQ EENEISMLQQ KEKEHLQV
Scfpep   Kkqpsltrav eniqin...e edNEISMLQe KErEfqeV
```

FIG. 16C



mAU AT 215 nm
300
200
100
0
10
20
30
40
50
TIME (MIN.)
C-terminal peptide

FIG. 16D

```
EcoRI
          ta  a   t   t   t a  a        t   t    c       g       t   a
GAATTCTTCCGTATCTTCAACCGTTCCATCGACGCTTTCAAAGACTTCGTT
E   F   F   R   I   F   N   R   S   I   D   A   F   K   D   F   V

  g   a   t        ta gt    t   t    g        t   a    at  a ag    t   g
GTTGCTTCCGAAACCTCCGACTGCGTTGTTTCCTCCACCCTGTCTCCGGAA
V   A   S   E   T   S   D   C   V   V   S   S   T   L   S   P   E

                           BstEII
       t    a  a   ca gt    c   a        a    t    t  a    c    t  .  a
AAAGACTCCCGTGTTTCGGTTACCAAACCGTTCATGCTGCCGCCGGTTGCT
K   D   S   R   V   S   V   T   K   P   F   M   L   P   P   V   A

  c ag          t a  g   t     ag   ag t ag  ag t    tag t   g      a   t
GCTTCCTCCCTGCGTAACGACTCCTCCTCCTCCAACTCCAAATACATCTAC
A   S   S   L   R   N   D   S   S   S   S   N   S   K   Y   I   Y

                     BamHI
     t
CTGATCTAATAGGATCC
L   I   •   •
```

FIG. 16E

BstEII

GGTTACCAAACCGTTCATGCTGCCGCCGGTTGCTGCTTAATAGGATCC BamHI

V T K P F M L P P V A A • •

FIG.17

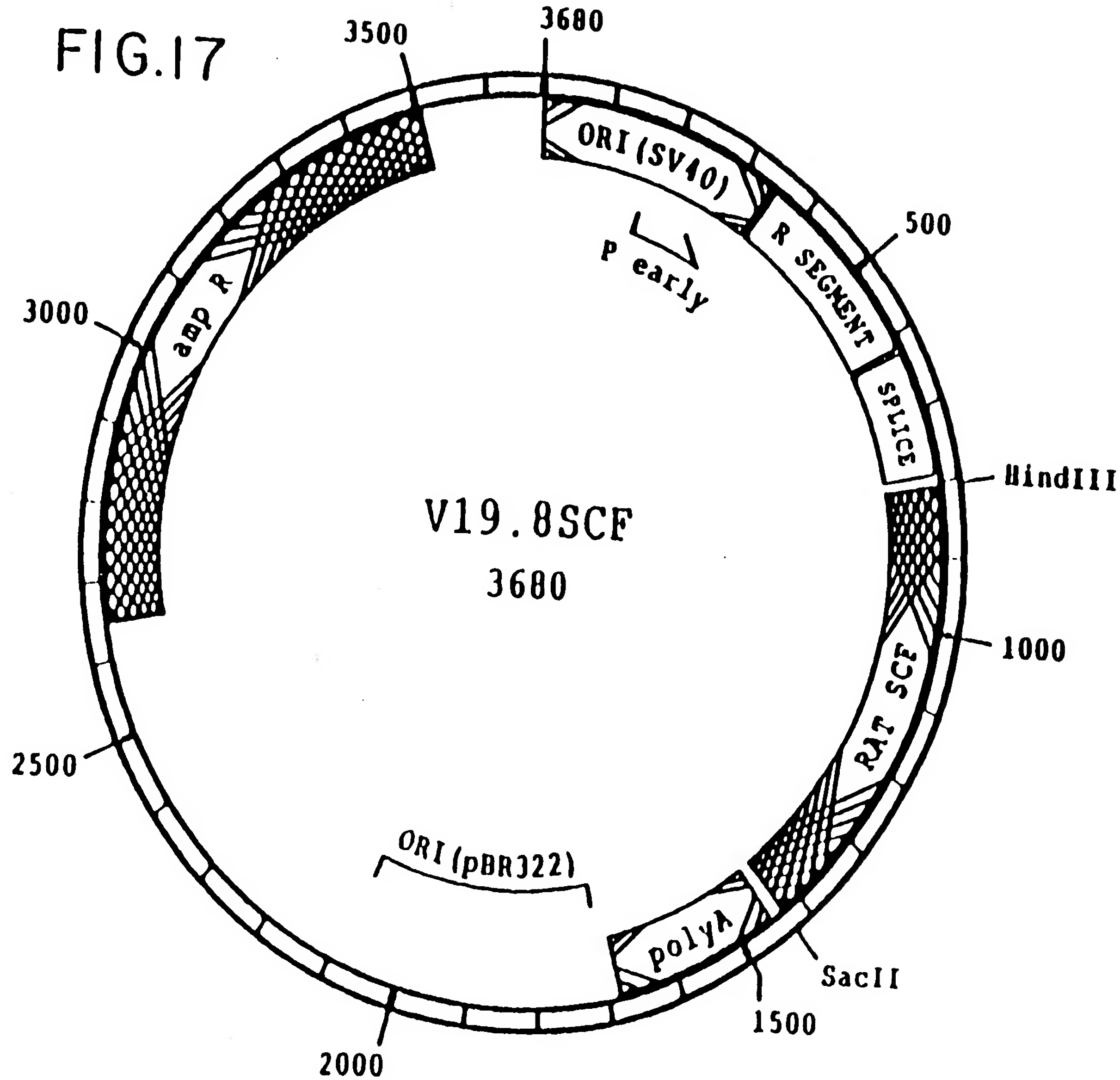

3680
3500
3000
2500
2000
1500
1000
500
HindIII
SacII
ORI(SV40)
P early
R SEGMENT
SPLICE
RAT SCF
polyA
ORI(pBR322)
amp R
V19.8SCF
3680

FIG.18

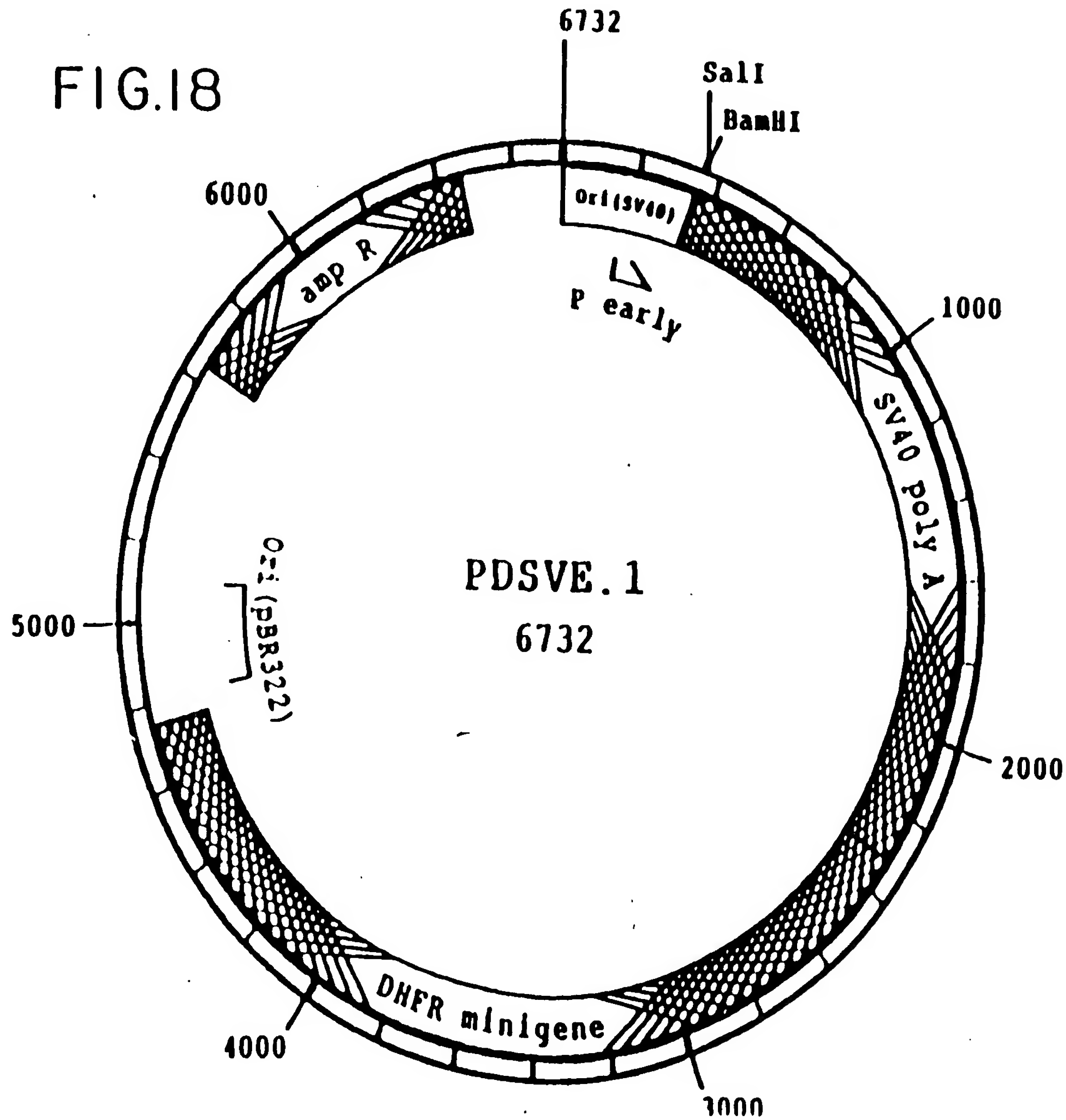

6732
SalI
BamHI
Ori(SV40)
P early
1000
SV40 poly A
2000
3000
DHFR minigene
4000
5000
Ori (pBR322)
6000
amp R
PDSVE.1
6732

FIG.19

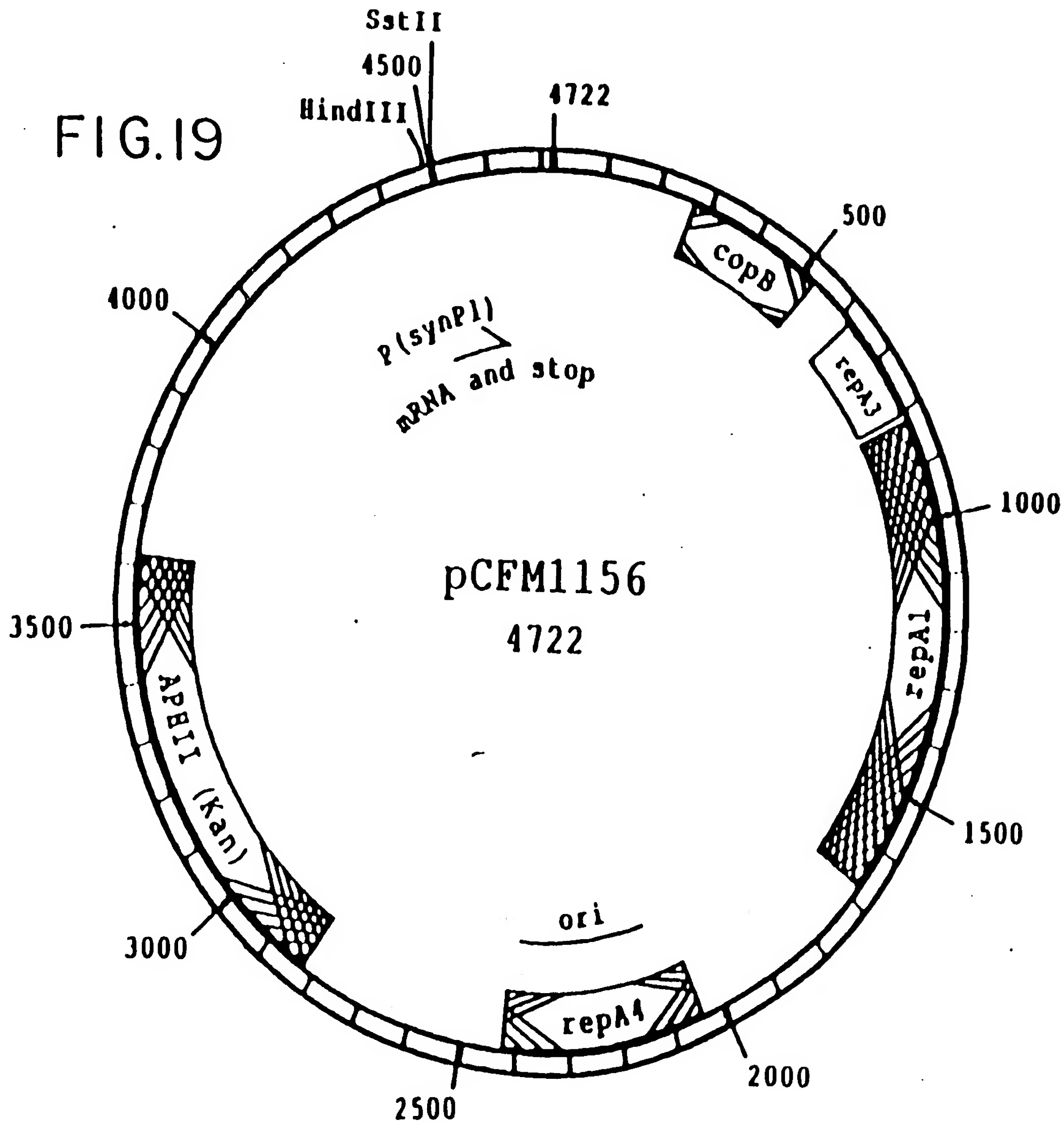
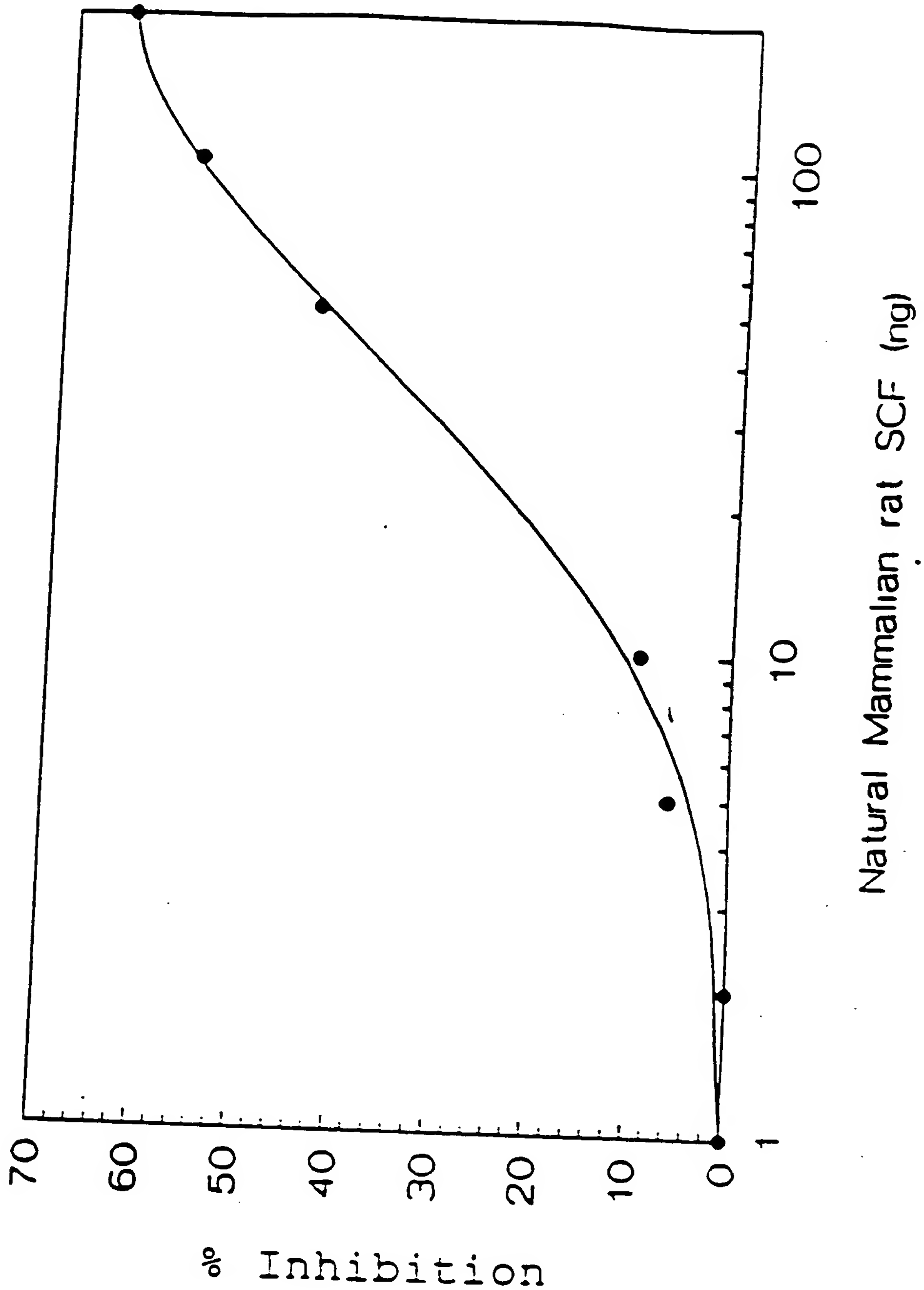

SstII
4500
HindIII
4722
500
copB
repA3
1000
repA1
1500
2000
repA4
ori
2500
3000
APHII (Kan)
3500
4000
P(synP1)
mRNA and stop
pCFM1156
4722

FIG.20A



% Inhibition
0
10
20
30
40
50
60
70
Natural Mammalian rat SCF (ng)
1
10
100

FIG. 20B

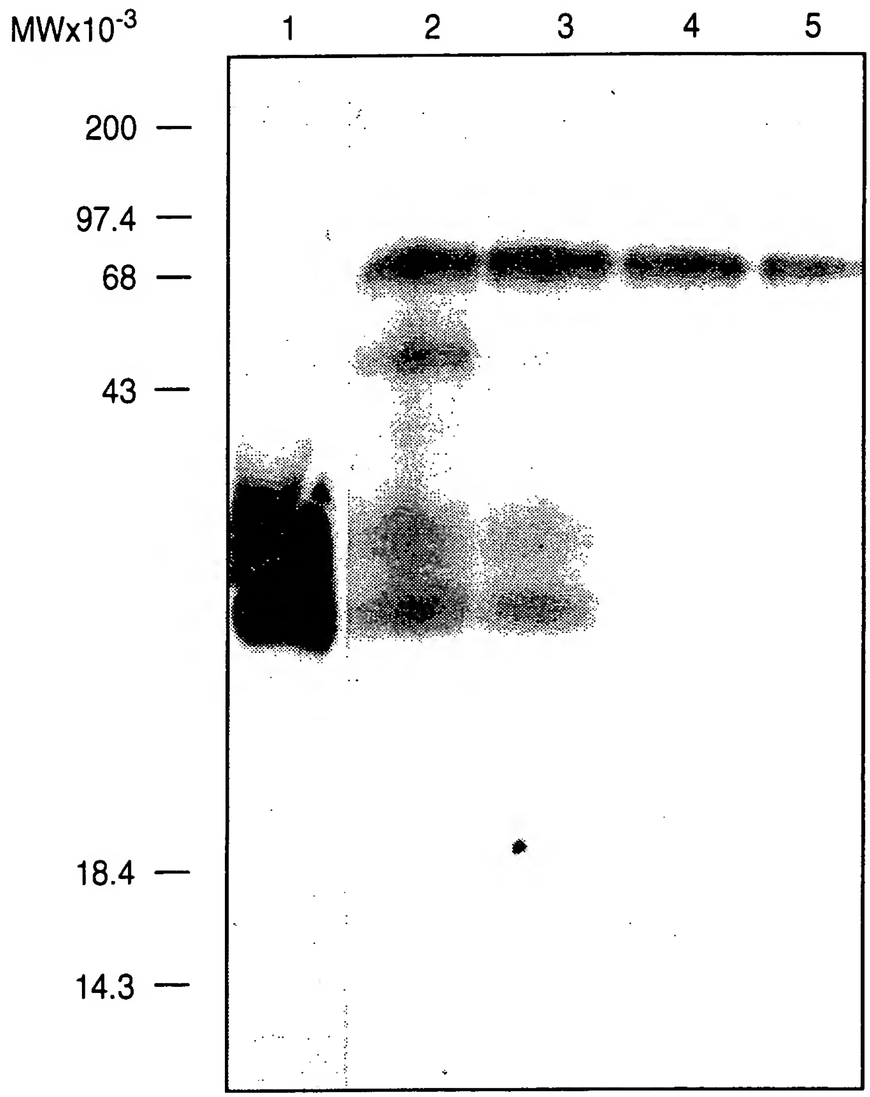


FIG. 21

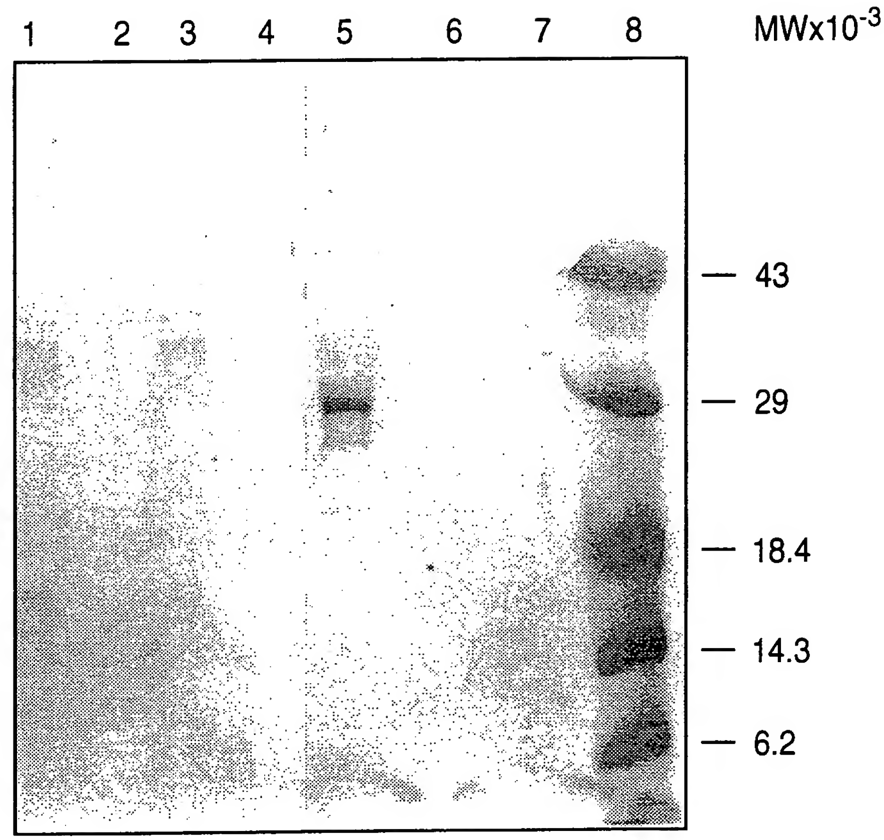


FIG. 22

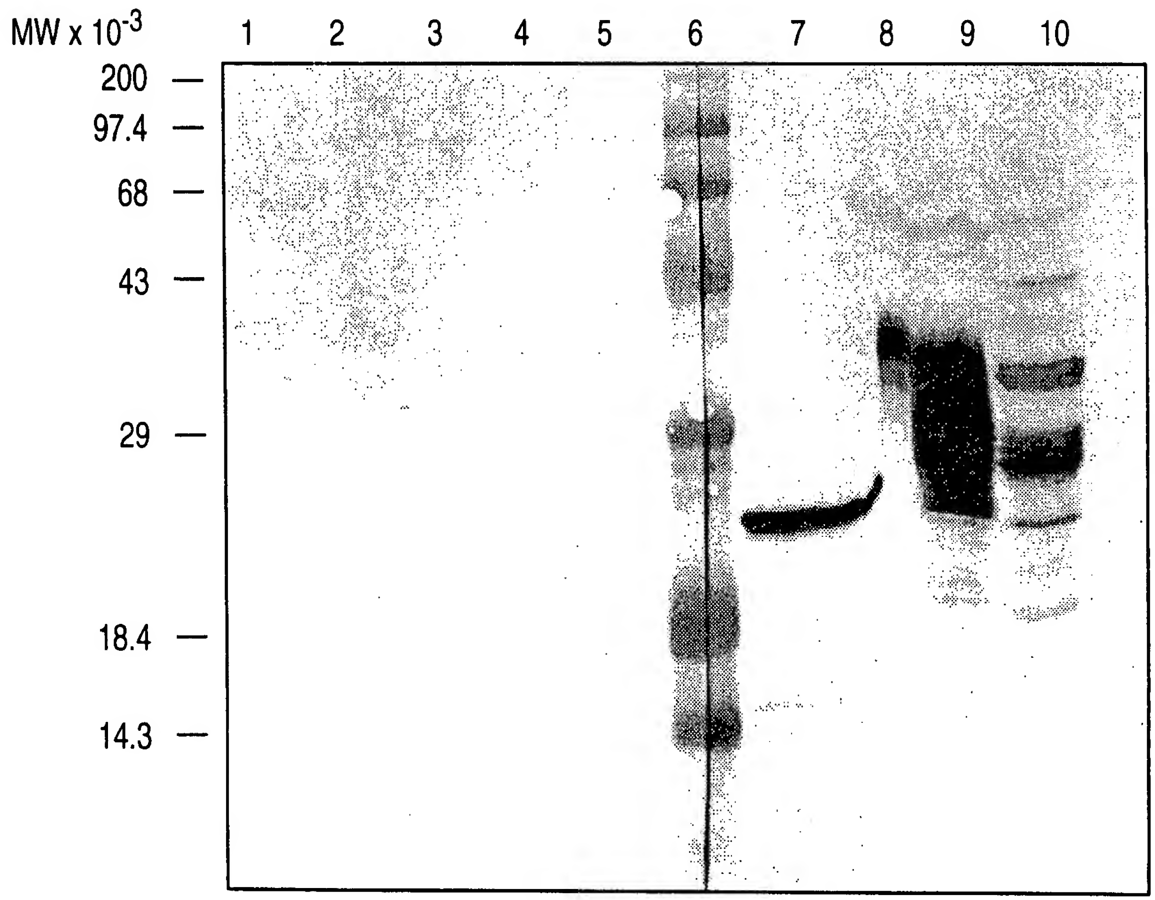


FIG. 22A

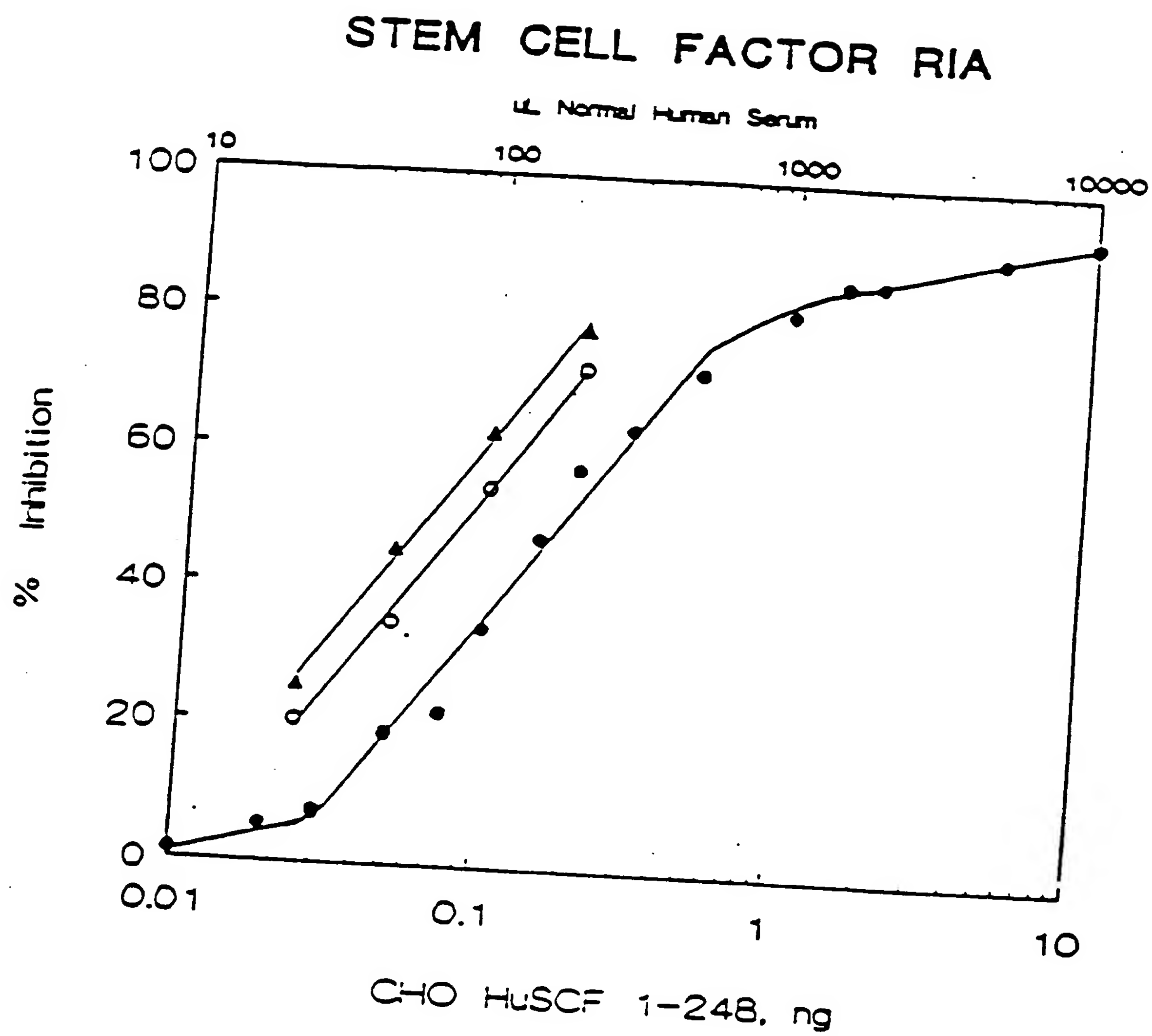
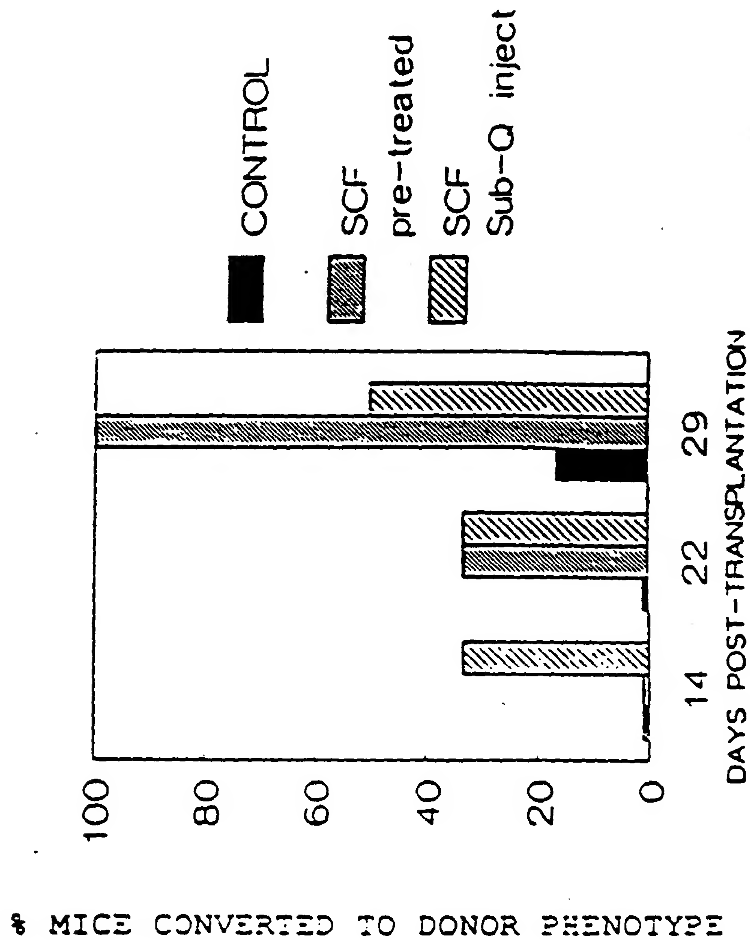

STEM CELL FACTOR RIA
uL Normal Human Serum
10
100
1000
10000
% Inhibition
100
80
60
40
20
0
0.01
0.1
1
10
CHO HuSCF 1-248, ng

FIG. 23



CONTROL
SCF pre-treated
SCF Sub-Q inject
100
80
60
40
20
0
14
22
29
DAYS POST-TRANSPLANTATION
% MICE CONVERTED TO DONOR PHENOTYPE

FIG. 24A

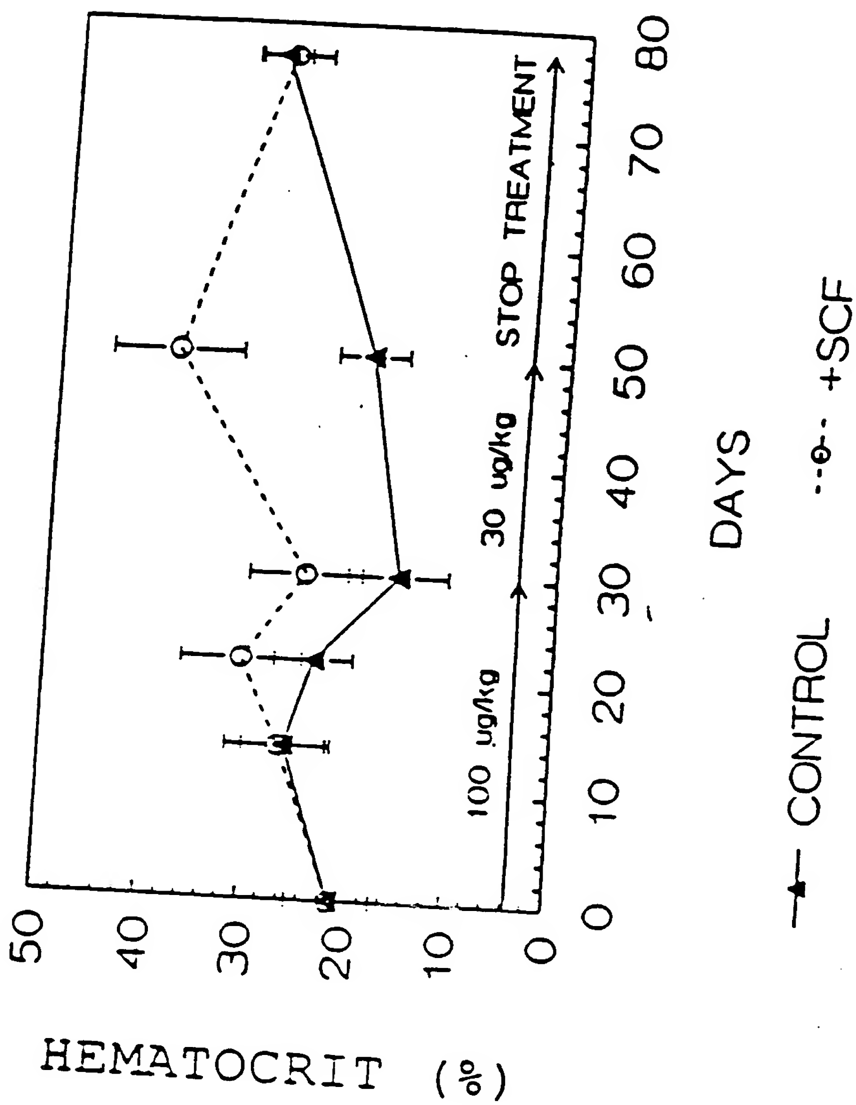
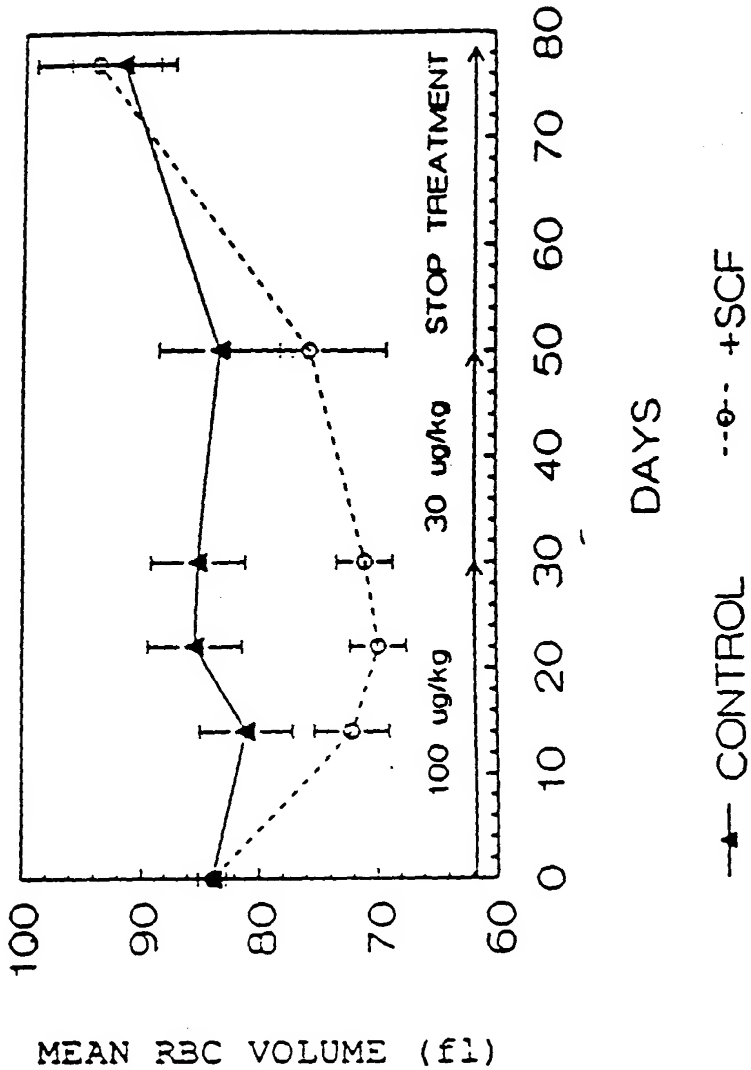
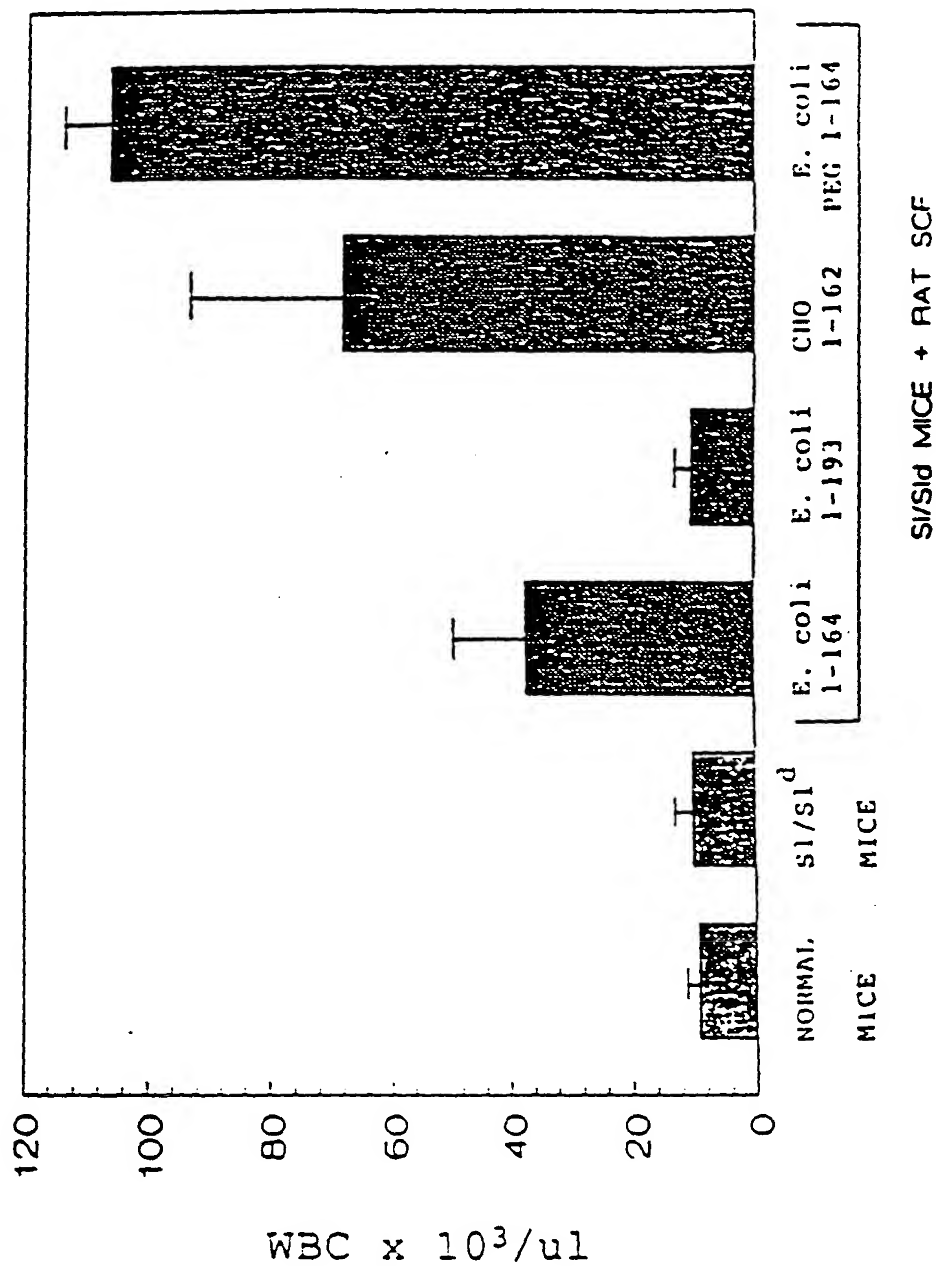

HEMATOCRIT (%)
0
10
20
30
40
50
DAYS
0
10
20
30
40
50
60
70
80
100 ug/kg
30 ug/kg
STOP TREATMENT
CONTROL
+SCF

FIG. 24B



100 ug/kg
30 ug/kg
STOP TREATMENT
0
10
20
30
40
50
60
70
80
DAYS
100
90
80
70
60
MEAN RBC VOLUME (fl)
CONTROL
+SCF

FIG. 25



WBC x 10³/ul
120
100
80
60
40
20
0
NORMAL MICE
Sl/Sl^d MICE
E. coli 1-164
E. coli 1-193
CHO 1-162
E. coli PEG 1-164
Sl/Sld MICE + RAT SCF

FIG.26

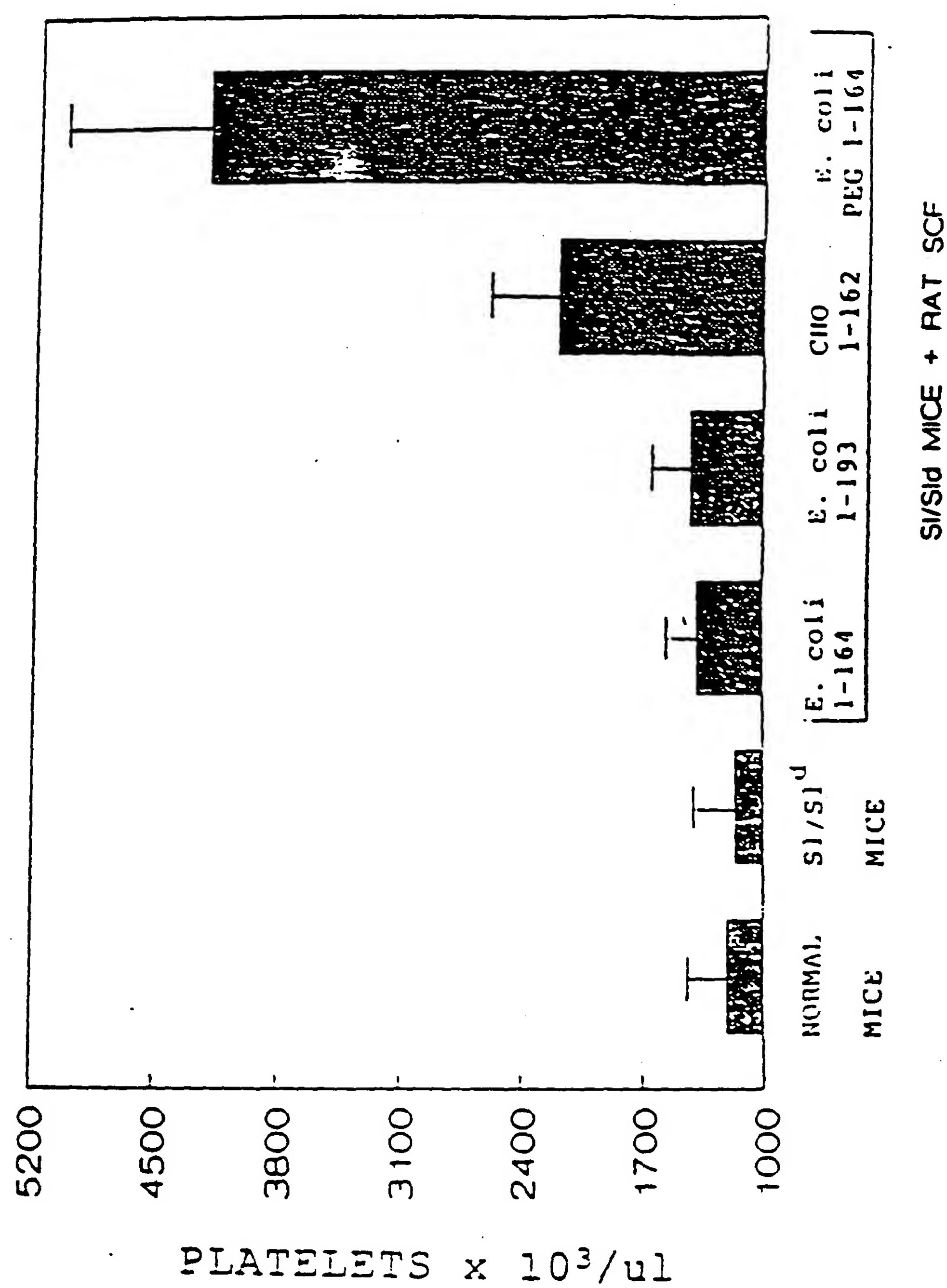
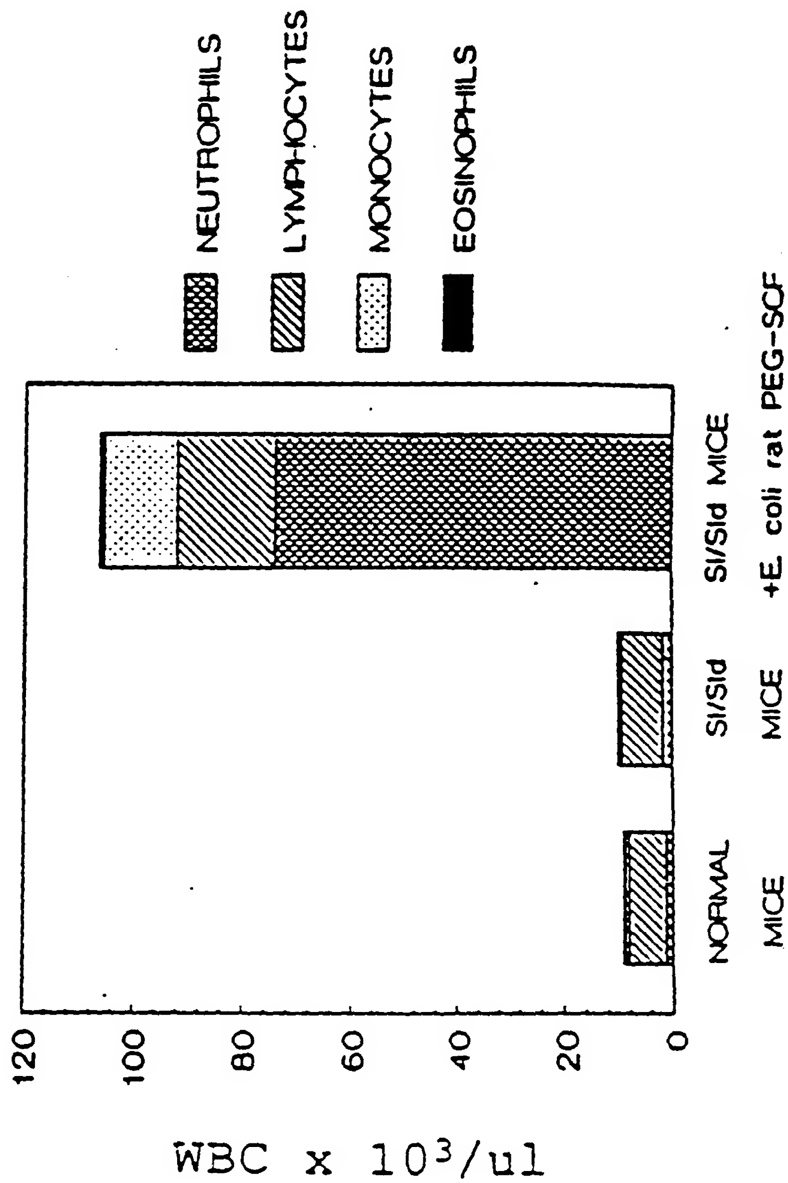
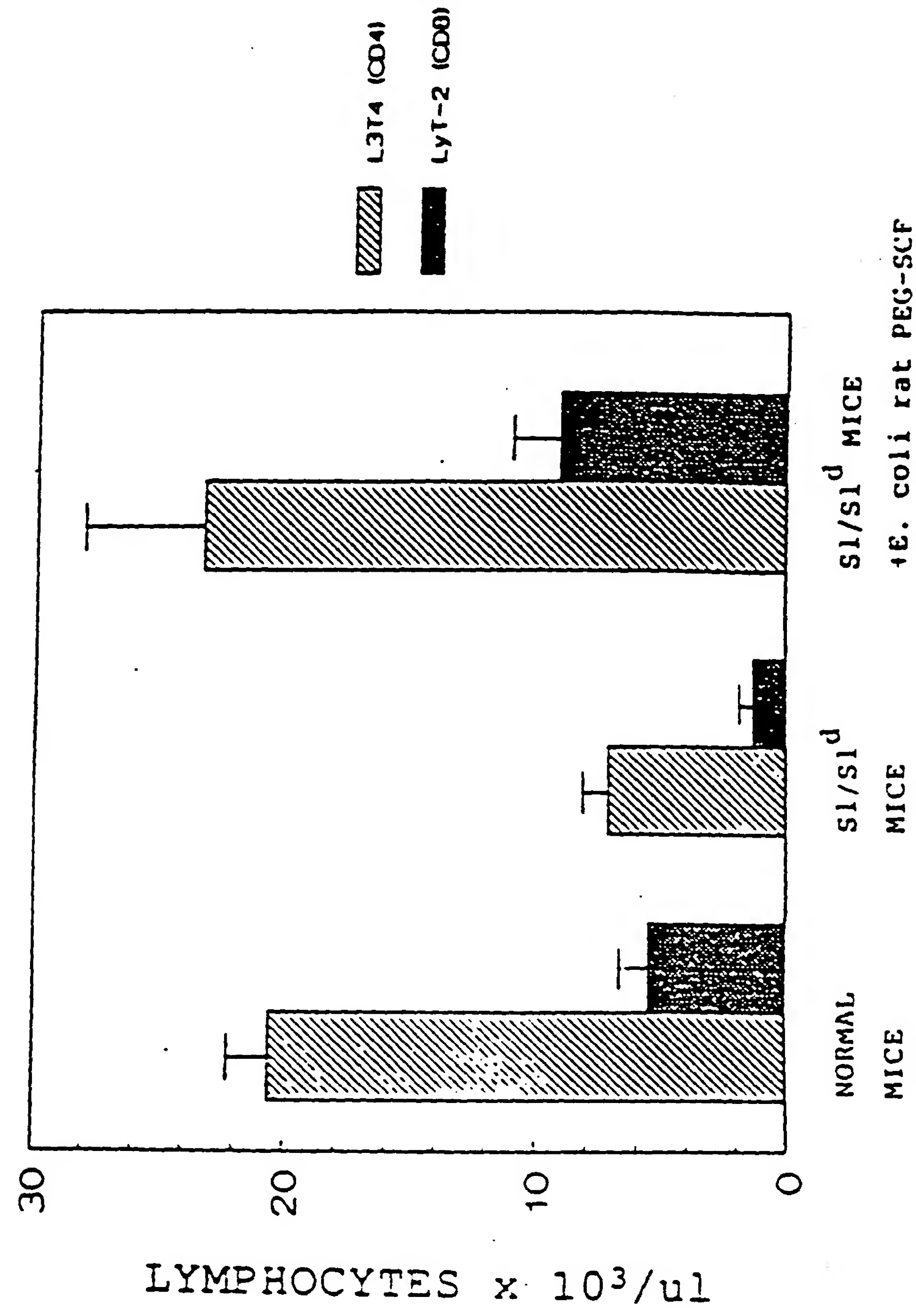

PLATELETS x 10³/ul
5200
4500
3800
3100
2400
1700
1000
NORMAL MICE
Sl/Sl^d MICE
E. coli 1-164
E. coli 1-193
CHO 1-162
E. coli PEG 1-164
Sl/Sld MICE + RAT SCF

FIG. 27



NEUTROPHILS
LYMPHOCYTES
MONOCYTES
EOSINOPHILS
WBC x 10³/ul
120
100
80
60
40
20
0
NORMAL MICE
Sl/Sld MICE
Sl/Sld MICE +E. coli rat PEG-SCF

FIG.28



L3T4 (CD4)
LyT-2 (CD8)
30
20
10
0
LYMPHOCYTES x 10³/ul
NORMAL MICE
Sl/Sl^d MICE
Sl/Sl^d MICE +E. coli rat PEG-SCF

FIG. 29A

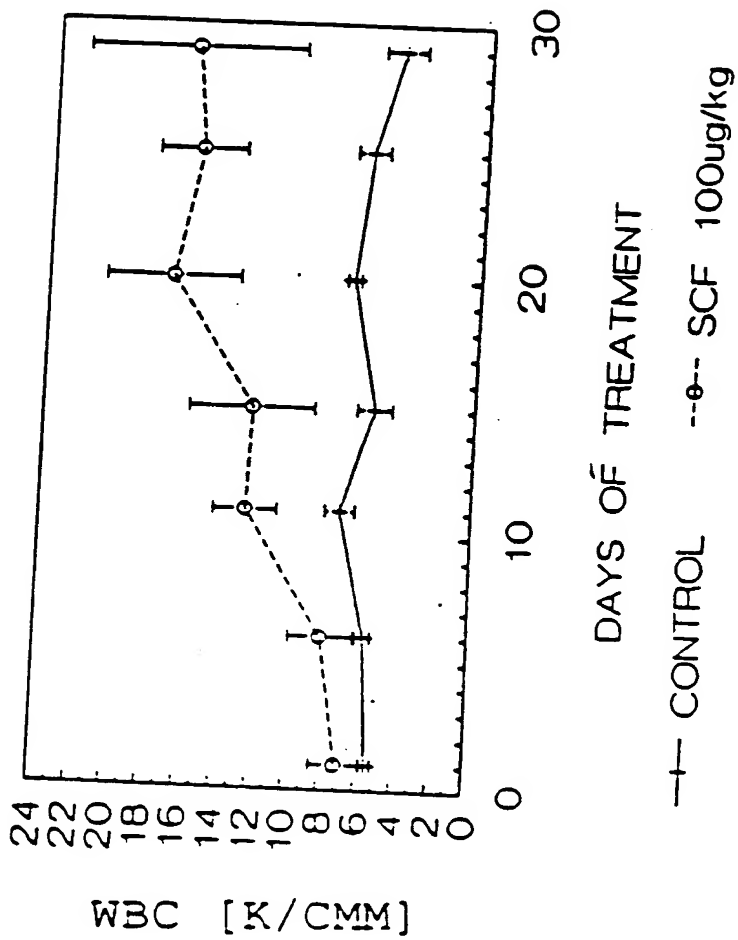
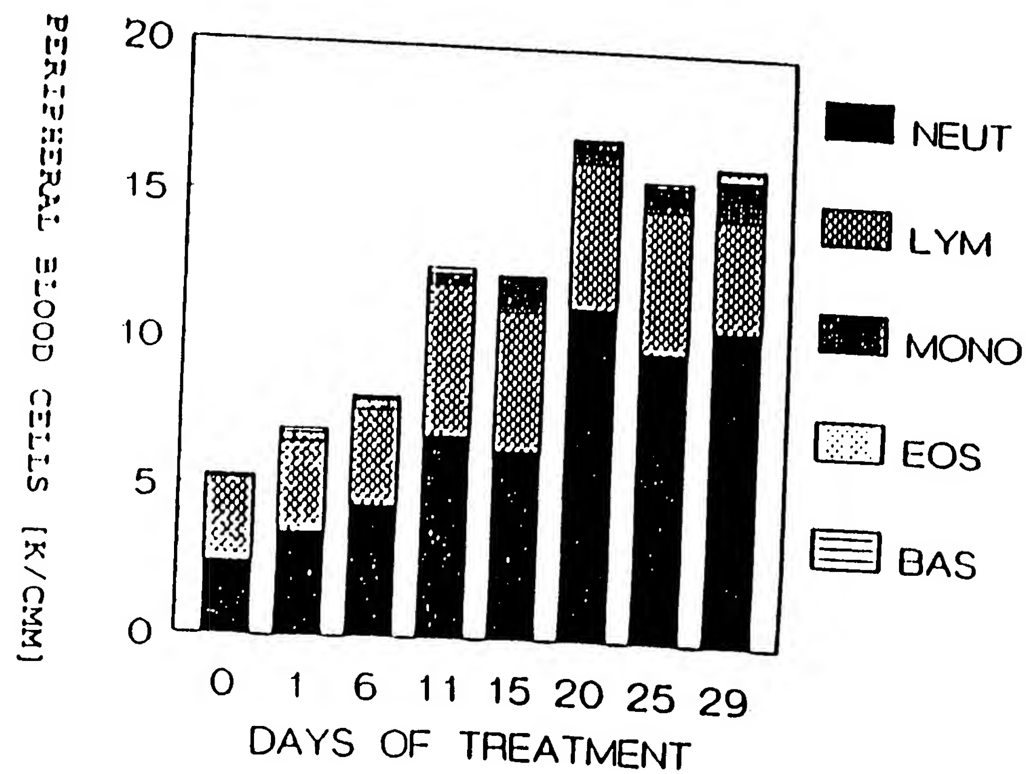
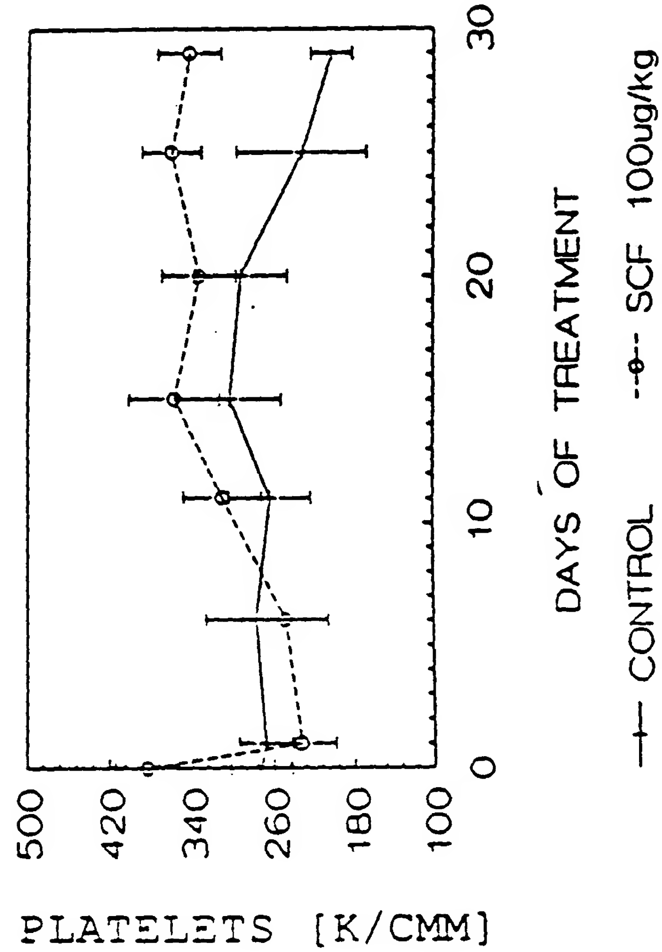

WBC [K/CMM]
0
2
4
6
8
10
12
14
16
18
20
22
24
0
10
20
30
DAYS OF TREATMENT
CONTROL
SCF 100ug/kg

FIG.29B



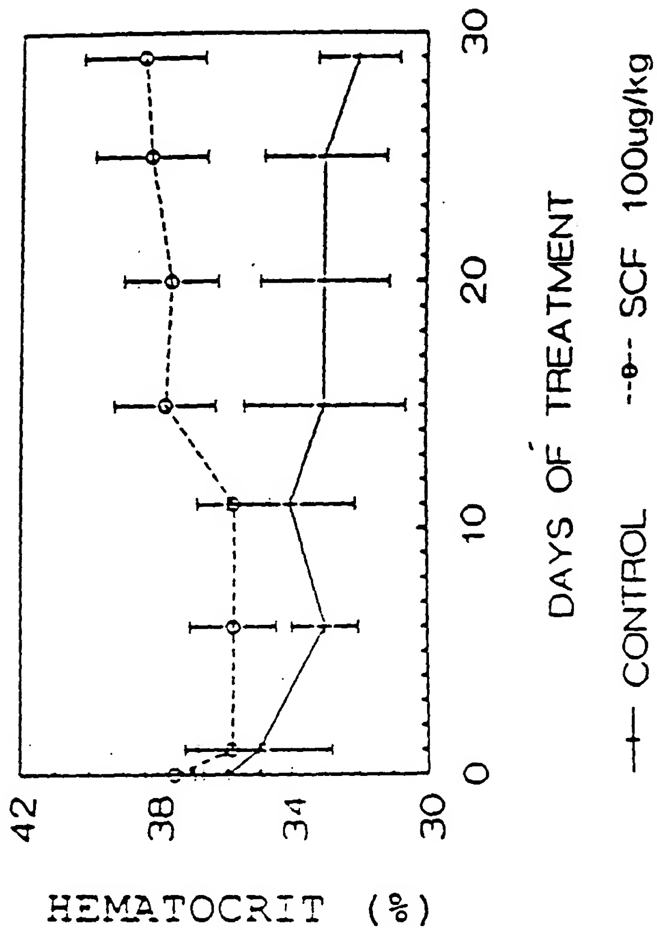
PERIPHERAL BLOOD CELLS [K/CMM]
20
15
10
5
0
0
1
6
11
15
20
25
29
DAYS OF TREATMENT
NEUT
LYM
MONO
EOS
BAS

FIG.30A



PLATELETS [K/CMM]
500
420
340
260
180
100
0
10
20
30
DAYS OF TREATMENT
CONTROL
SCF 100ug/kg

FIG.30B



HEMATOCRIT (%)
42
38
34
30
0
10
20
30
DAYS OF TREATMENT
CONTROL
SCF 100ug/kg

FIG. 31A

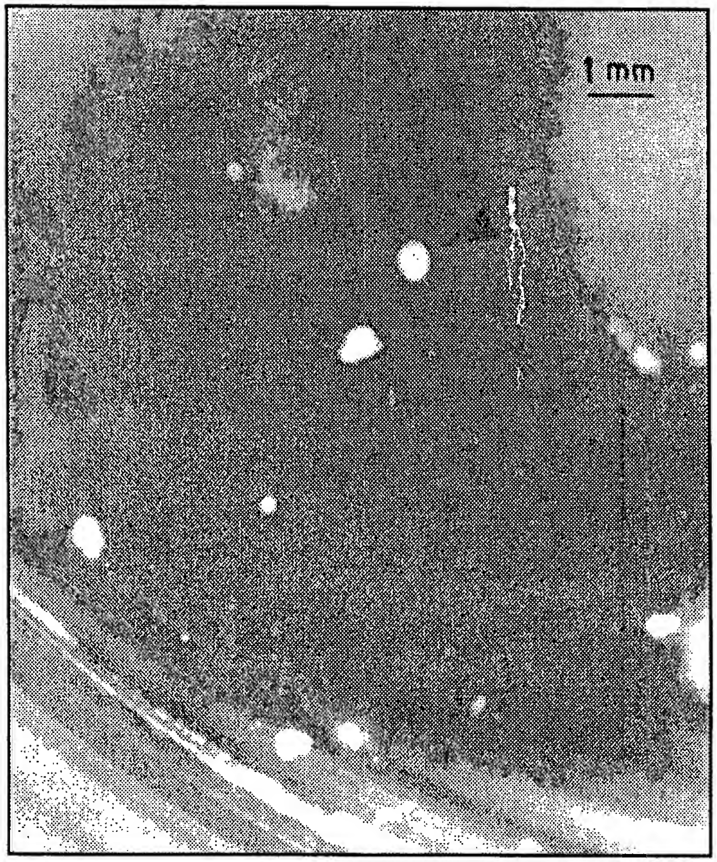


FIG. 31B

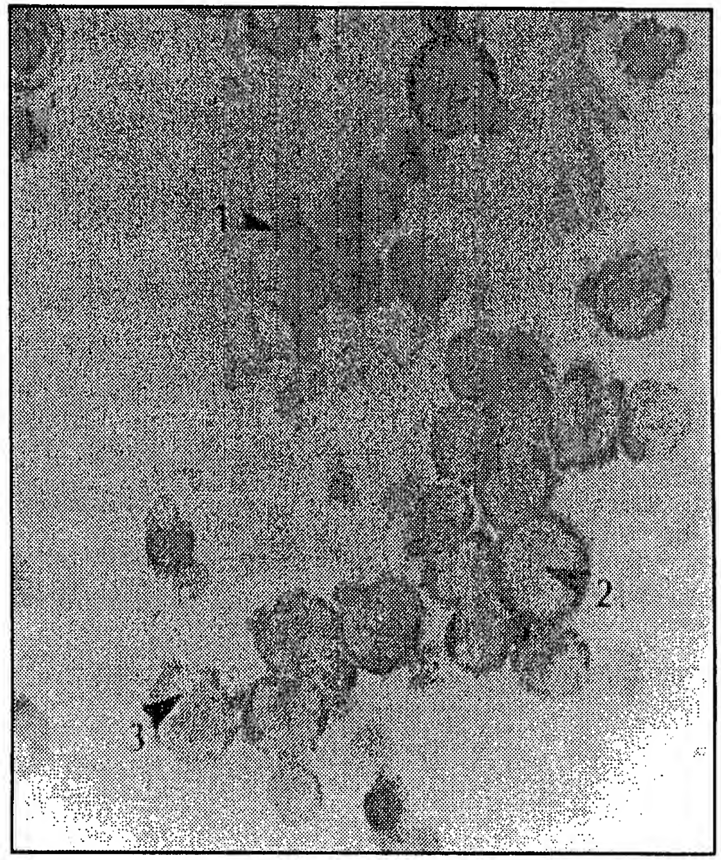


FIG. 31C

SCF4 SMP4

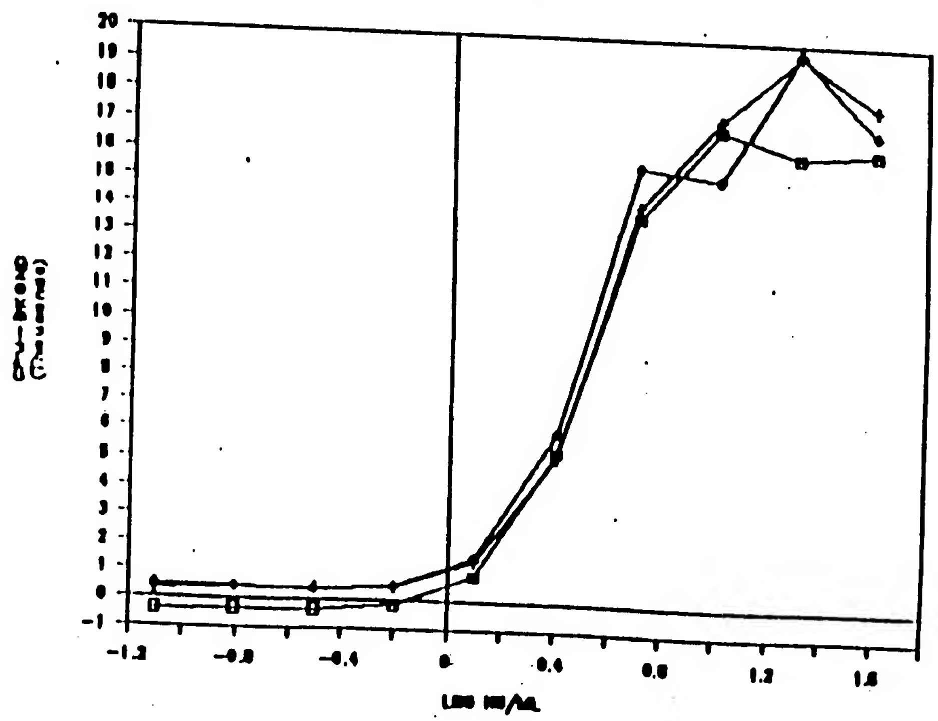


FIG. 32A

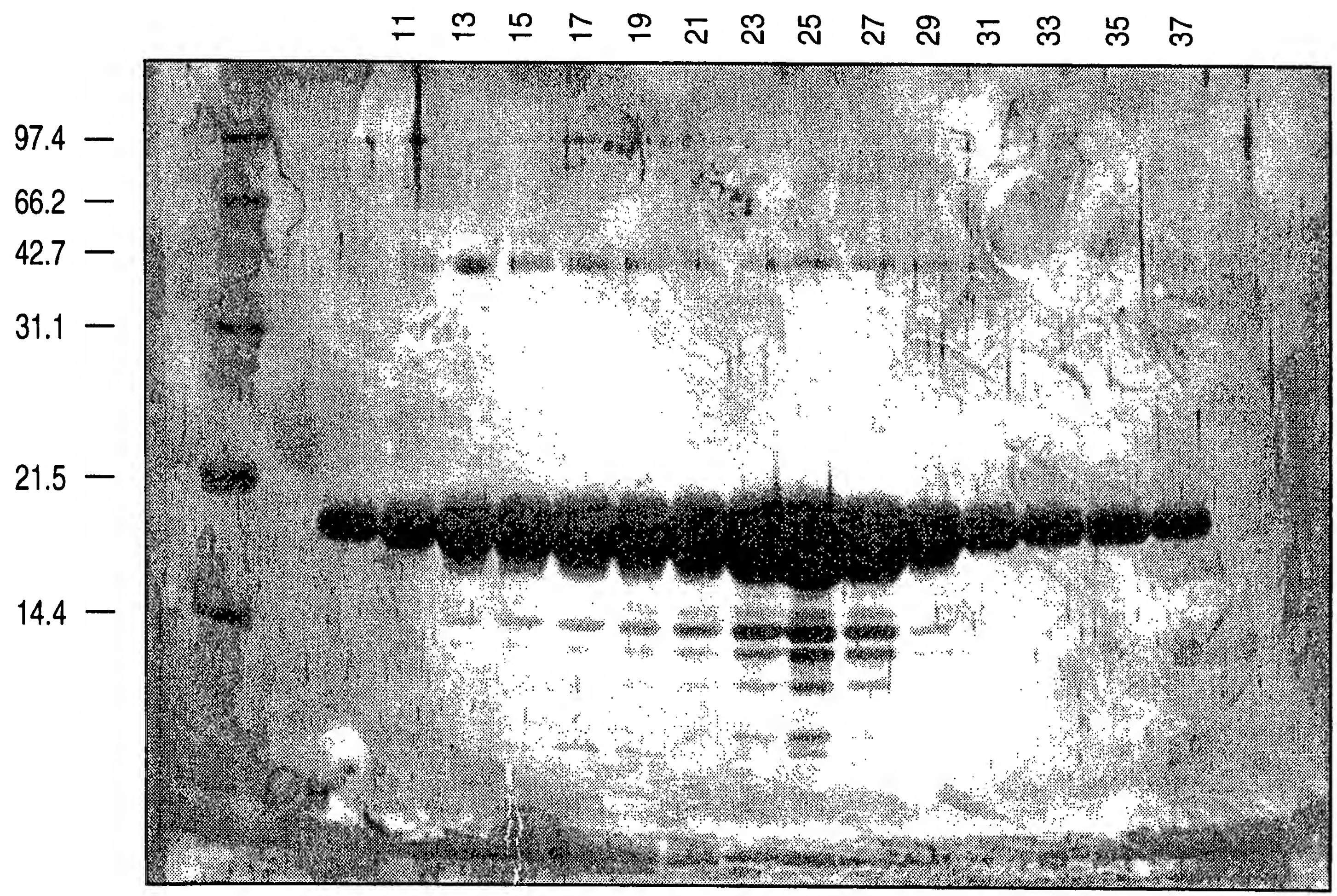


FIG. 32B

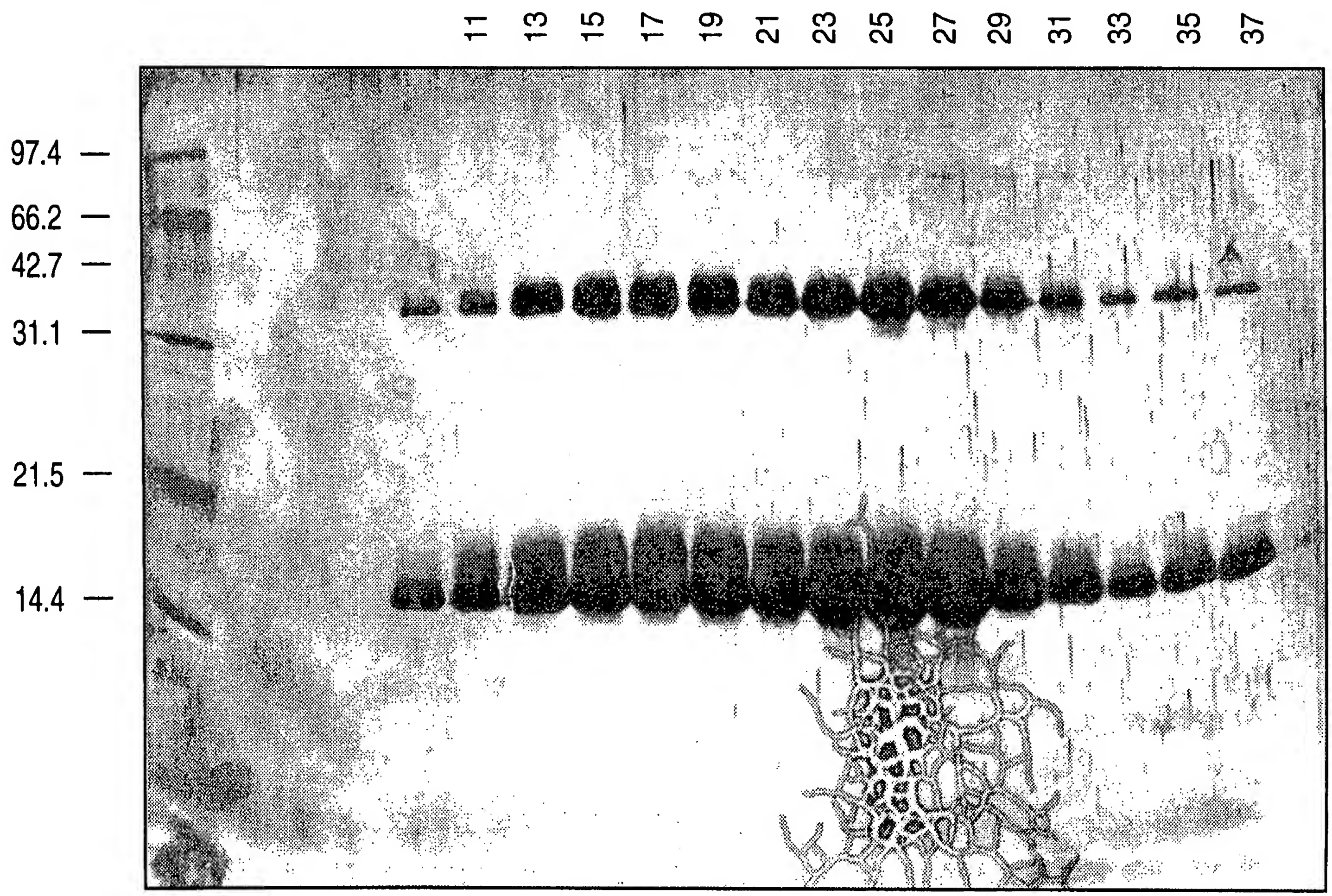
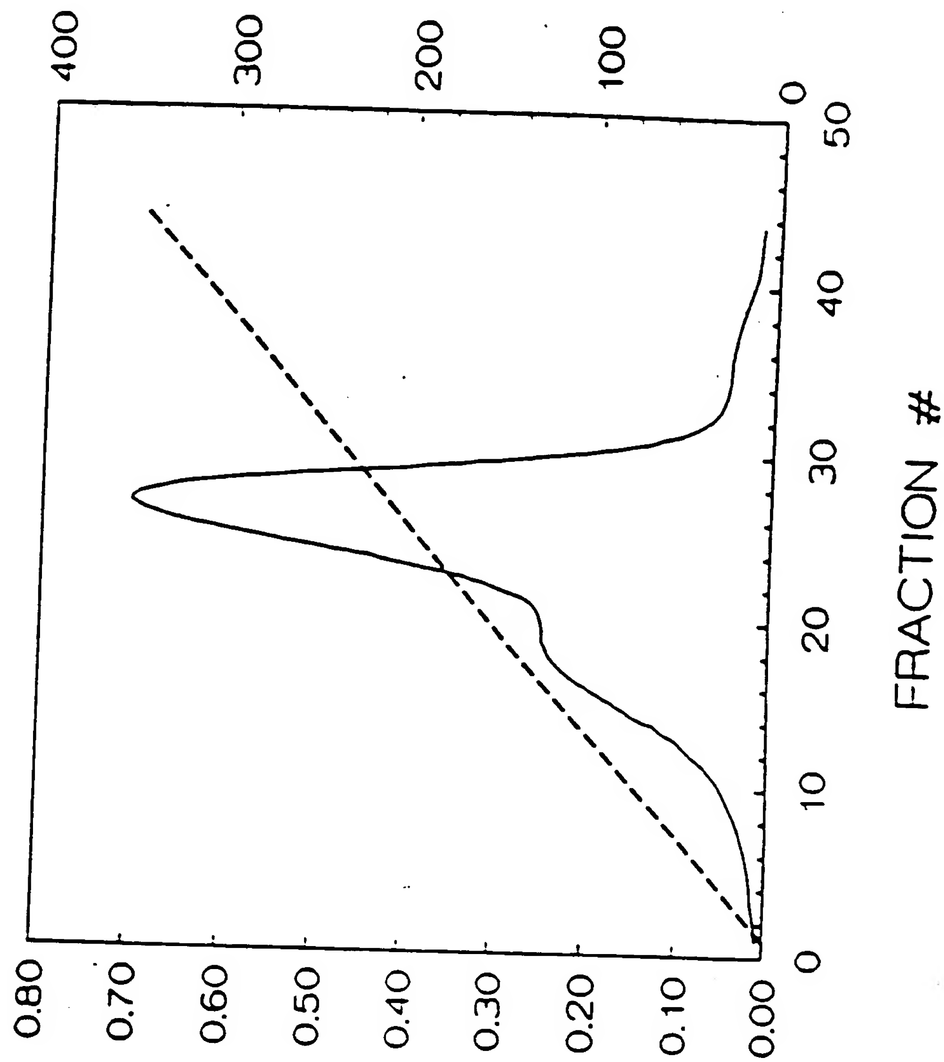


FIG.33

NaCl (mM) -----



O.D. 280nm ——

FIG. 34A

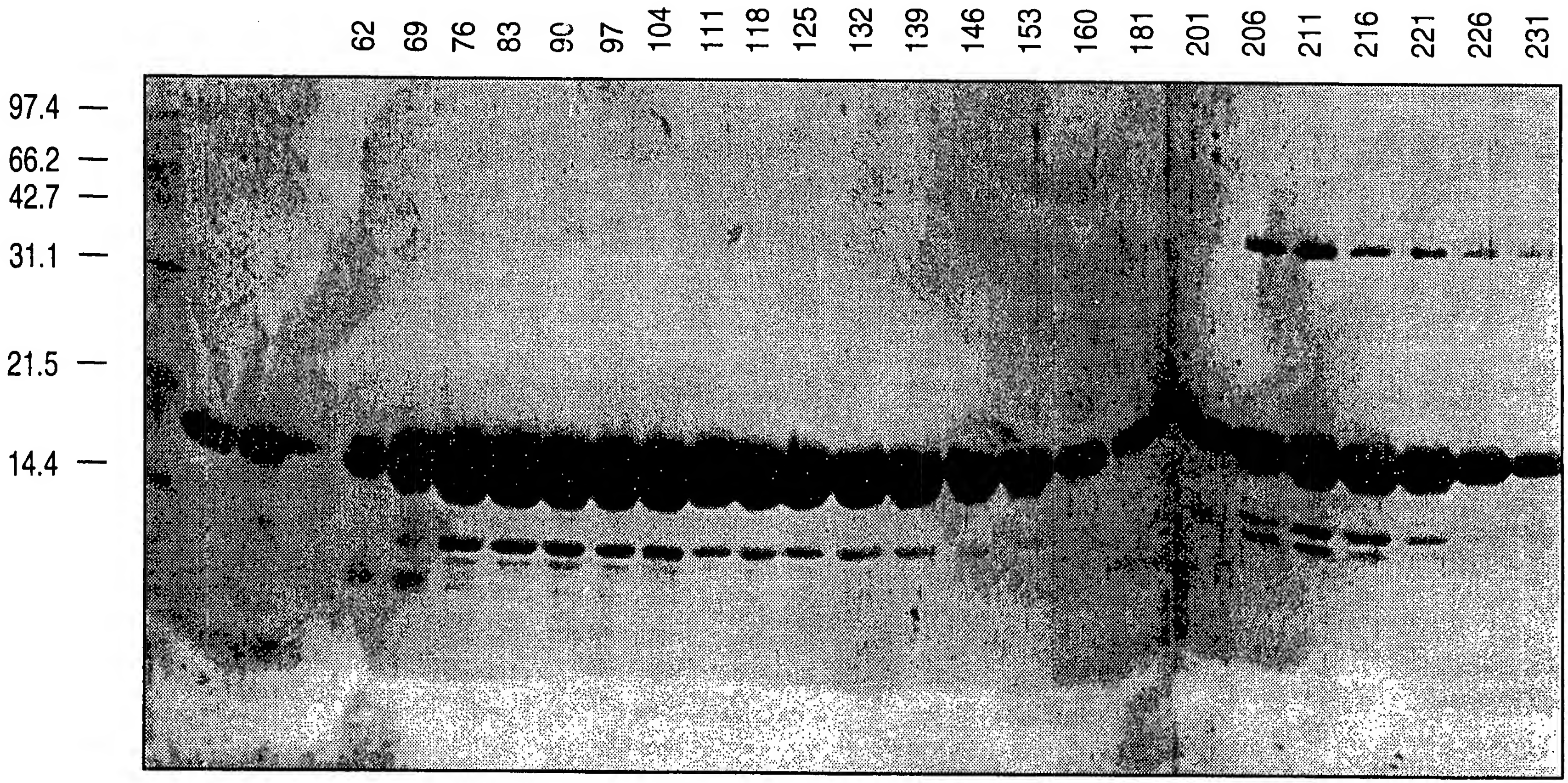

62
69
76
83
90
97
104
111
118
125
132
139
146
153
160
181
201
206
211
216
221
226
231
97.4
66.2
42.7
31.1
21.5
14.4

FIG. 34B

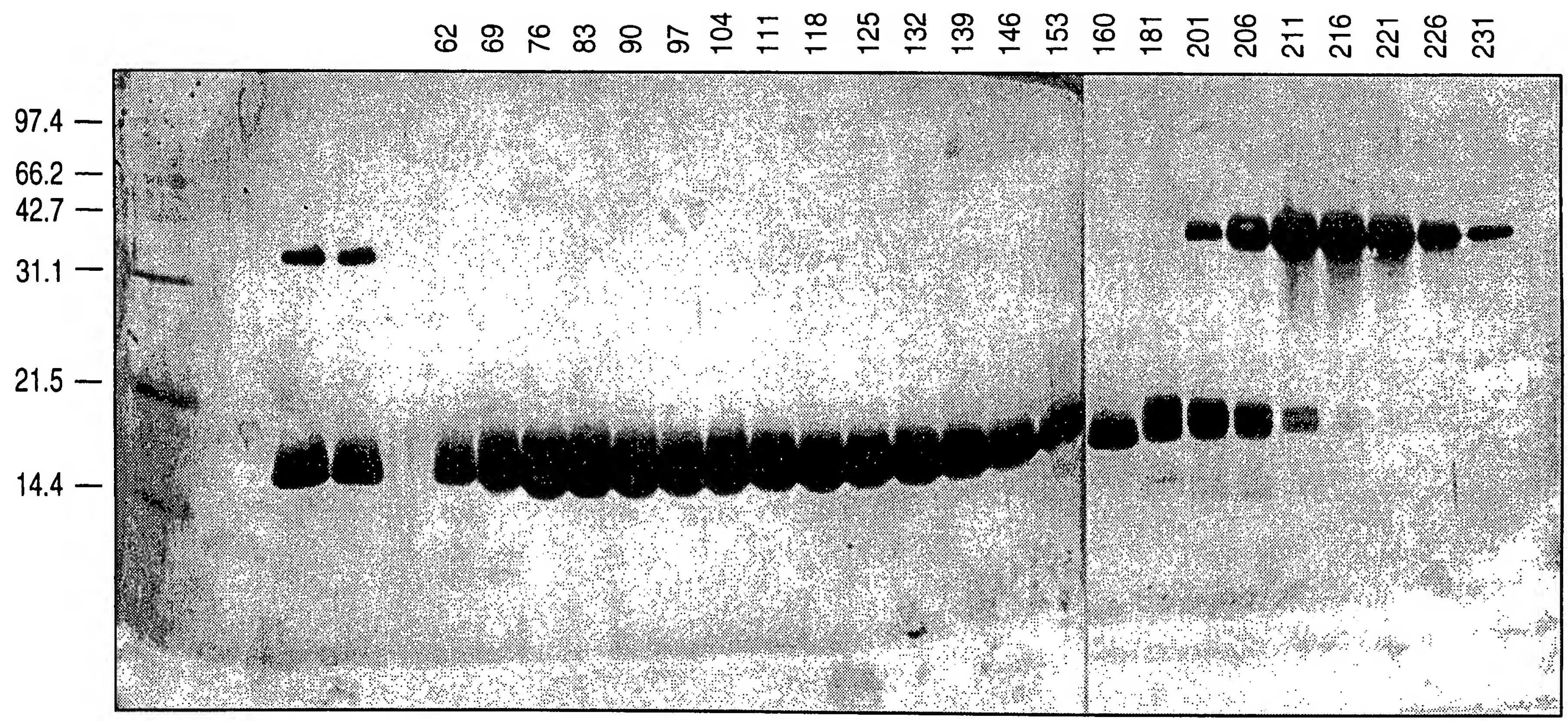

62
69
76
83
90
97
104
111
118
125
132
139
146
153
160
181
201
206
211
216
221
226
231
97.4
66.2
42.7
31.1
21.5
14.4

FIG.35

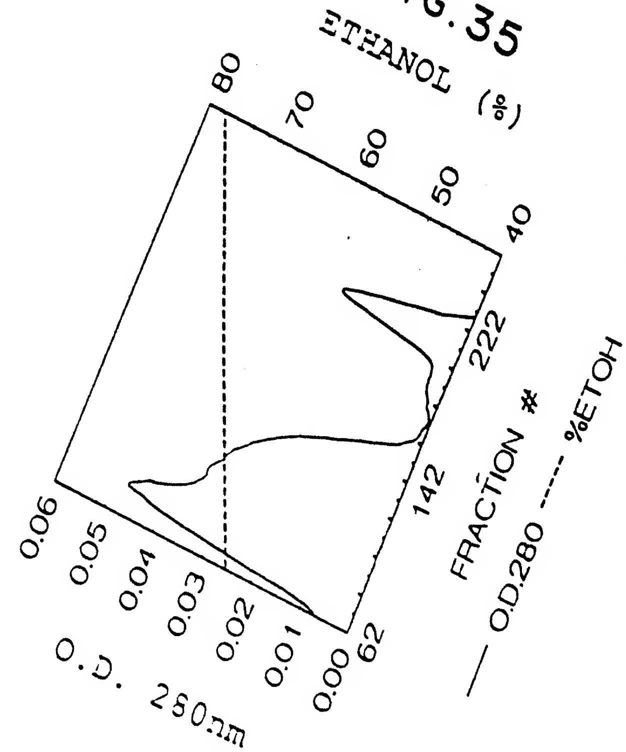
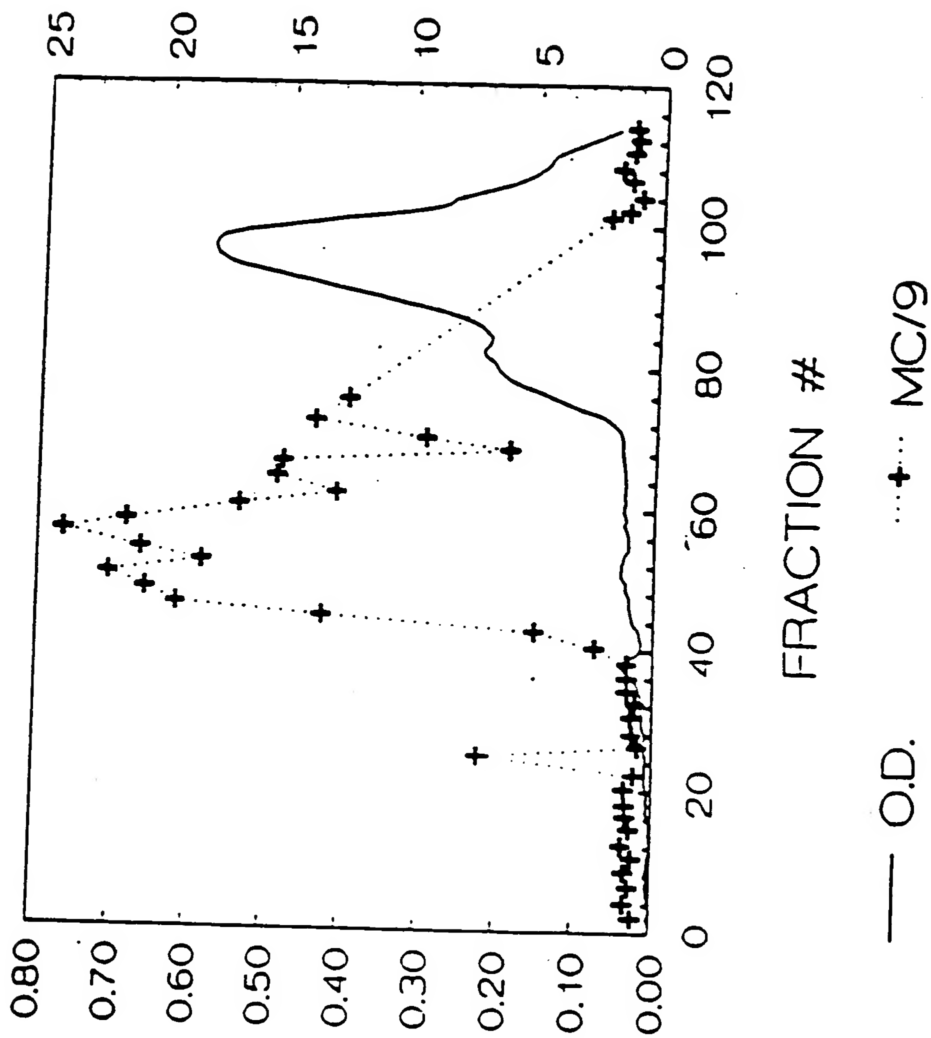

ETHANOL (%)
80
70
60
50
40
222
142
62
FRACTION #
— O.D.280 ----- %ETOH
0.06
0.05
0.04
0.03
0.02
0.01
0.00
O.D. 280nm

FIG. 36

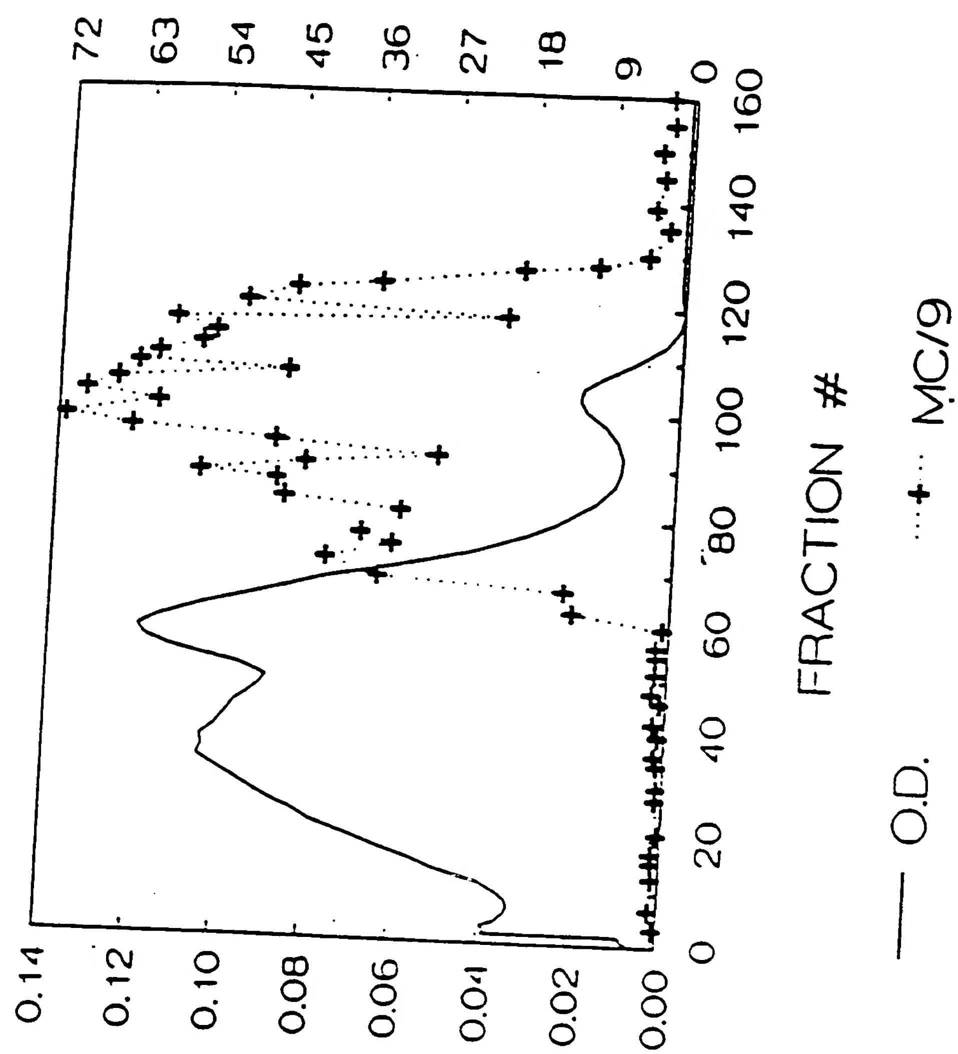
MC/9 CPM $(x\ 10^{-3})$



O.D. 280nm

FIG. 37

MC/9 CPM ($\times 10^{-3}$)



O.D. 280nm ($\times 10^{1}$)

FIG. 38

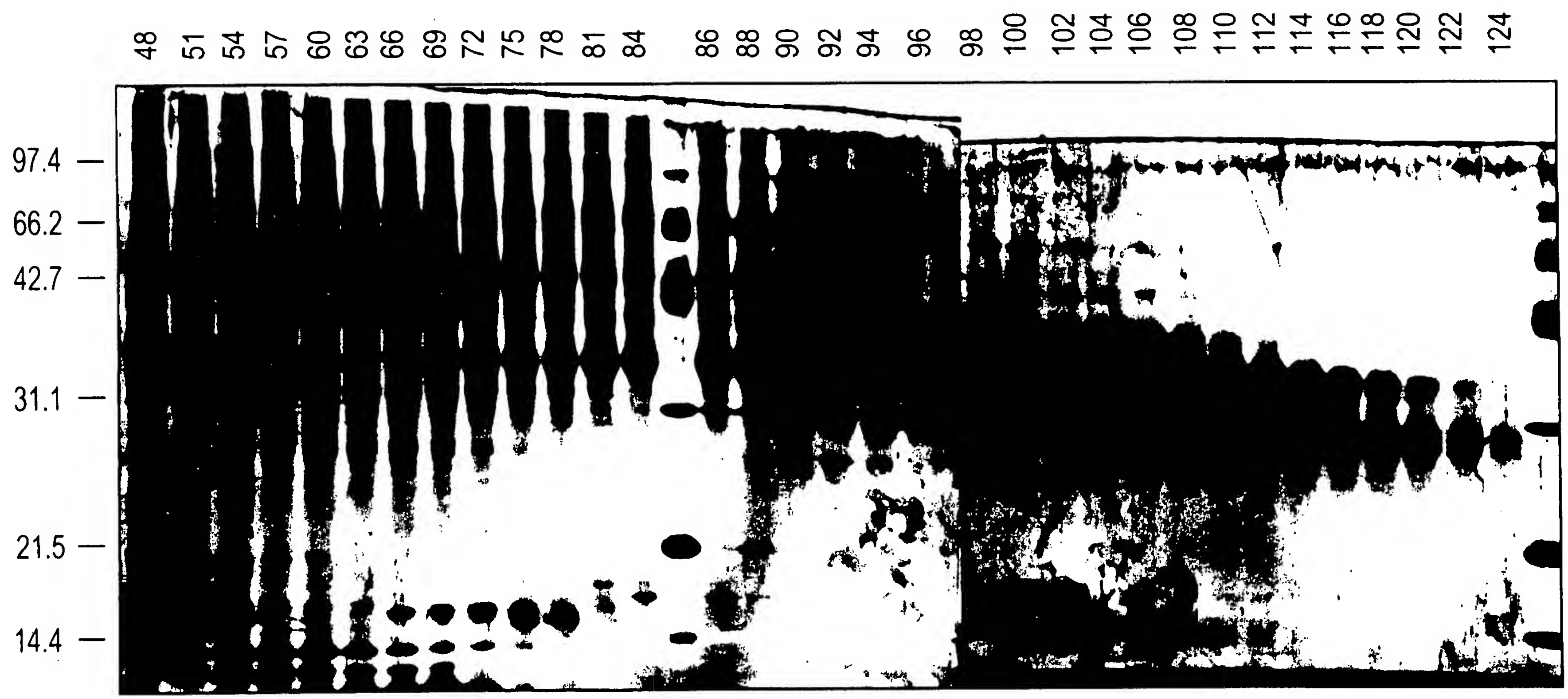

48
51
54
57
60
63
66
69
72
75
78
81
84
86
88
90
92
94
96
98
100
102
104
106
108
110
112
114
116
118
120
122
124
97.4
66.2
42.7
31.1
21.5
14.4

FIG. 39

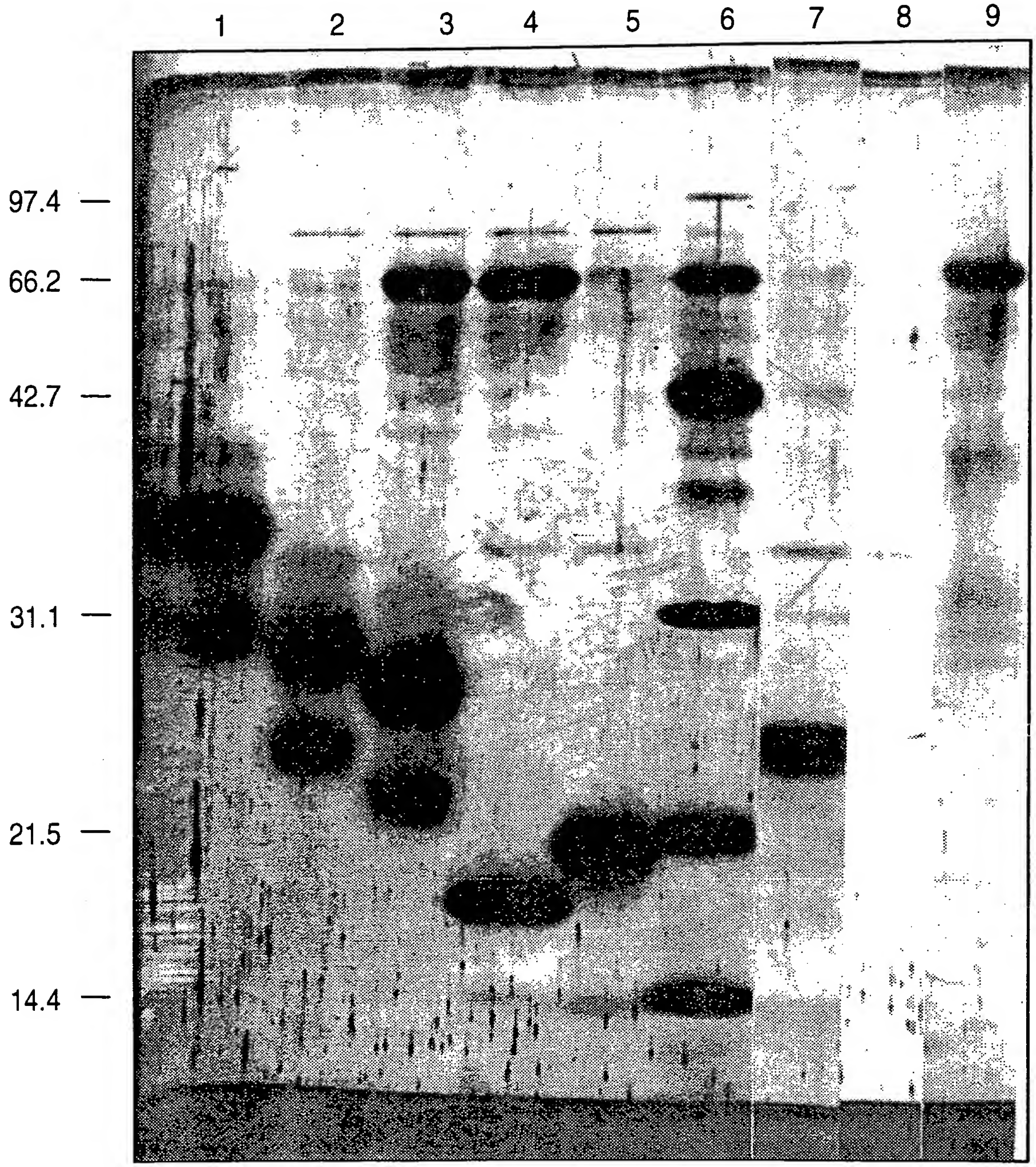


FIG. 40A

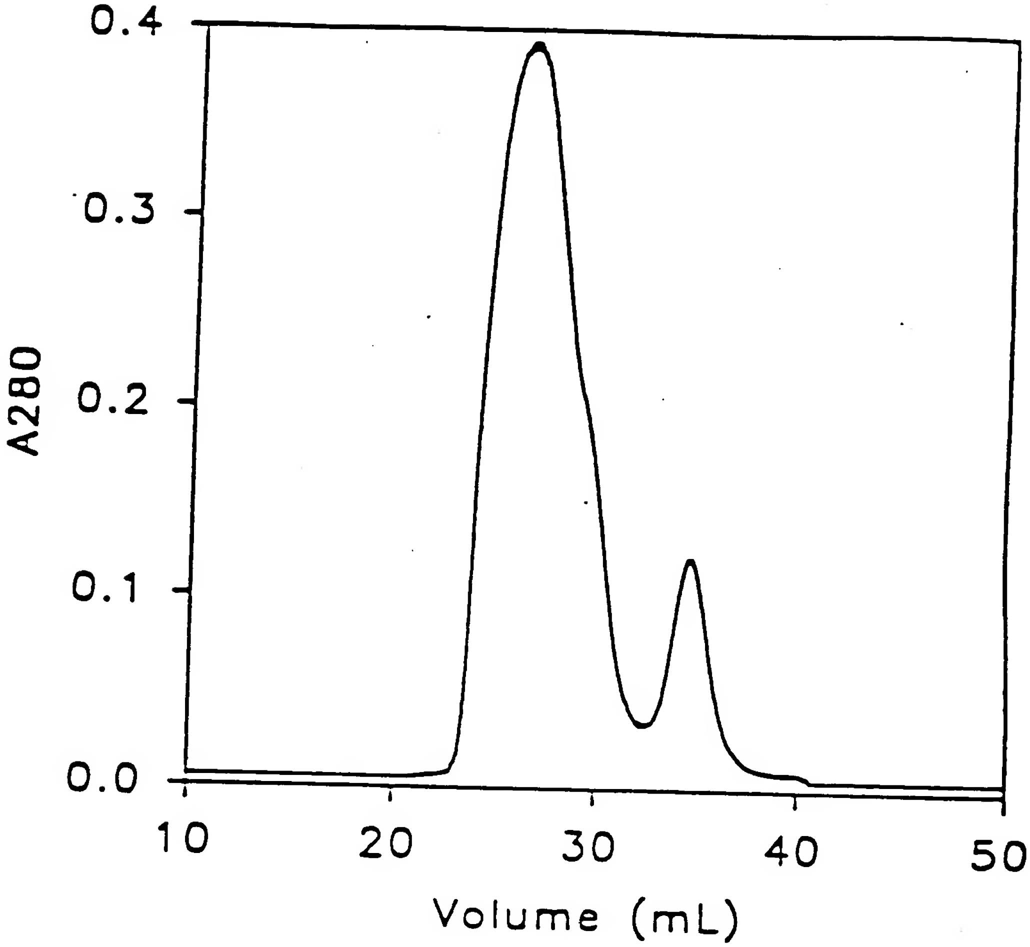


FIG. 40B

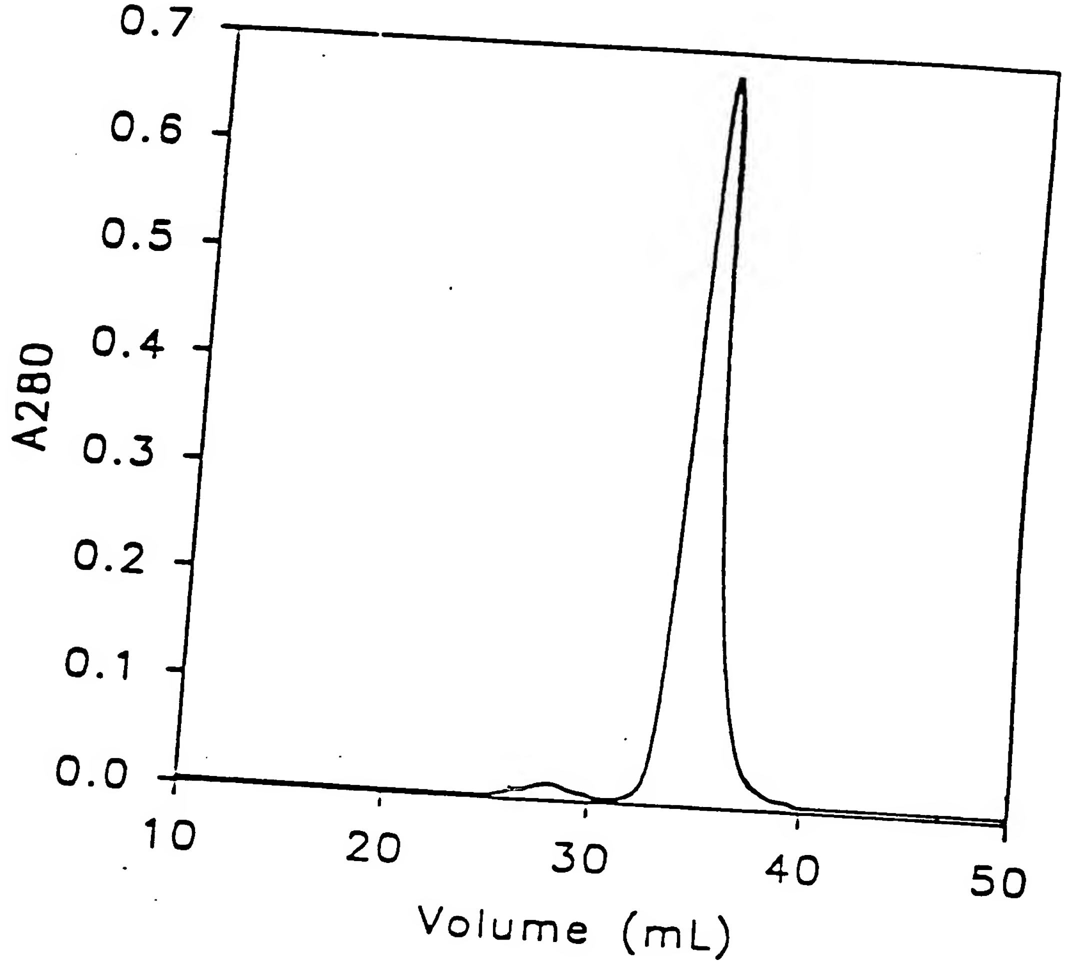
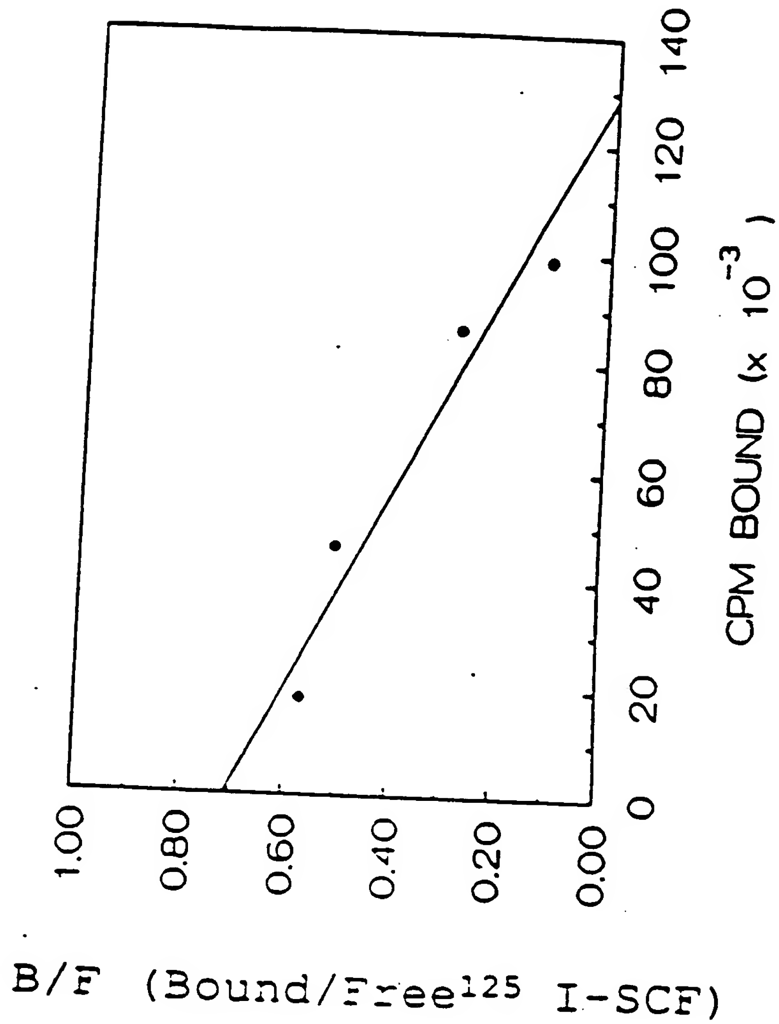


FIG. 41



1.00
0.80
0.60
0.40
0.20
0.00
B/F (Bound/Free125 I-SCF)
0
20
40
60
80
100
120
140
CPM BOUND (x 10-3)

FIG.42A

```
CCGCCTCGCGCCGAGACTAGAAGCGCTGCGGGAAGCAGGGACAGTGGAGAGGGCGCTGCGC   61

TCGGGCTACCCAATGCGTGGACTATCTGCCGCCGCTGTTCGTGCAATATGCTGGAGCTCCA  122

GAACAGCTAAACGGAGTCGCCACACCACTGTTTGTGCTGGATCGCAGCGCTGCCTTTCCTT  183

-25                 -20
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln
ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG     228

-10                                     1
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg
CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG     273

                10                                      20
Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala
AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA     318

                                    30
Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly
AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG     363

                40                                      50
Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val
ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA     408

                                    60
Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT     453
```

FIG.42B

```
                                 70                                      80
Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val
ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG   498

                                                   90
Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser
AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT   543

                100                                     110
Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe
AAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT   588

                                           120
Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala
ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC   633

                130                                     140
Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val
TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT   678

                                           150
Ser Ser Thr Leu Ser Pro Glu Lys Asp Ser Arg Val Ser Val Thr
TCT TCA ACA TTA AGT CCT GAG AAA GAT TCC AGA GTC AGT GTC ACA   723
```

FIG.42C

```
                    160                                          170
Lys Pro Phe Met Leu Pro Pro Val Ala Ala Ser Ser Leu Arg Asn
AAA CCA TTT ATG TTA CCC CCT GTT GCA GCC AGC TCC CTT AGG AAT    768

                                        180
Asp Ser Ser Ser Ser Asn Arg Lys Ala Lys Asn Pro Pro Gly Asp
GAC AGC AGT AGC AGT AAT AGG AAG GCC AAA AAT CCC CCT GGA GAC    813

                    190                                          200
Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu Phe Ser
TCC AGC CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG TTT TCT    858

                                        210
Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys Lys Arg
CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG AAG AGA    903

                    220                                          230
Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile Asn Glu
CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT AAT GAA    948

                                    240
Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg Glu Phe
GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA GAG TTT    993

        248
Gln Glu Val End
CAA GAA GTG TAA     TTGTGGCTTGTATCAACACTGTTACTTTCGTACATTGGC 1044
```

FIG.42D

TGGTAACAGTTCATGTTTGCTTCATAAATGAAGCAGCTTTAAACAAATTCATATTCTGTC 1104

TGGAGTGACAGACCACATCTTTATCTGTTCTTGCTACCCATGACTTTATATGGATGATTC 1164

AGAAATTGGAACAGAATGTTTTACTGTGAAACTGGCACTGAATTAATCATCTATAAAGAA 1224

GAACTTGCATGGAGCAGGACTCTATTTTAAGGACTGCGGGACTTGGGTCTCATTTAGAAC 1284

TTGCAGCTGATGTTGGAAGAGAAAGCACGTGTCTCAGACTGCATGTACCATTTGCATGGC 1344

TCCAGAAATGTCTAAATGCTGAAAAAACACCTAGCTTTATTCTTCAGATACAAACTGCAG 1404

FIG. 43

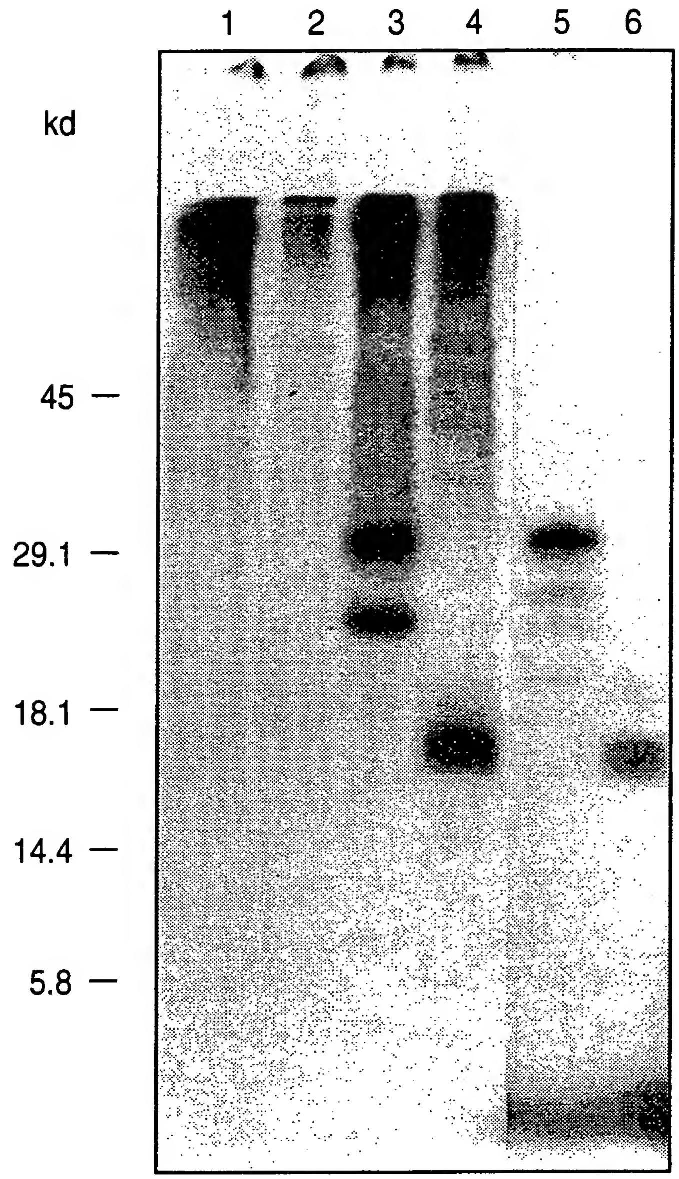


FIG. 44A

```
                              AGCAGGGACAGTGGAGAGGGCGCTGCGCTC   30

GGGCTACCCAATGCGTGGACTATCTGCCGCCGCTGTTCGTGCAATATGCTGGAGCTCCAG   90

AACAGCTAAACGGAGTCGCCACACCACTGTTTGTGCTGGATCGCAGCGCTGCCTTTCCTT  150

-25                 -20
Met Lys Lys Thr Gln Thr Trp Ile Leu Thr Cys Ile Tyr Leu Gln
ATG AAG AAG ACA CAA ACT TGG ATT CTC ACT TGC ATT TAT CTT CAG   195

-10                                     1
Leu Leu Leu Phe Asn Pro Leu Val Lys Thr Glu Gly Ile Cys Arg
CTG CTC CTA TTT AAT CCT CTC GTC AAA ACT GAA GGG ATC TGC AGG   240

                10                                      20
Asn Arg Val Thr Asn Asn Val Lys Asp Val Thr Lys Leu Val Ala
AAT CGT GTG ACT AAT AAT GTA AAA GAC GTC ACT AAA TTG GTG GCA   285

                                    30
Asn Leu Pro Lys Asp Tyr Met Ile Thr Leu Lys Tyr Val Pro Gly
AAT CTT CCA AAA GAC TAC ATG ATA ACC CTC AAA TAT GTC CCC GGG   330

                40                                      50
Met Asp Val Leu Pro Ser His Cys Trp Ile Ser Glu Met Val Val
ATG GAT GTT TTG CCA AGT CAT TGT TGG ATA AGC GAG ATG GTA GTA   375
```

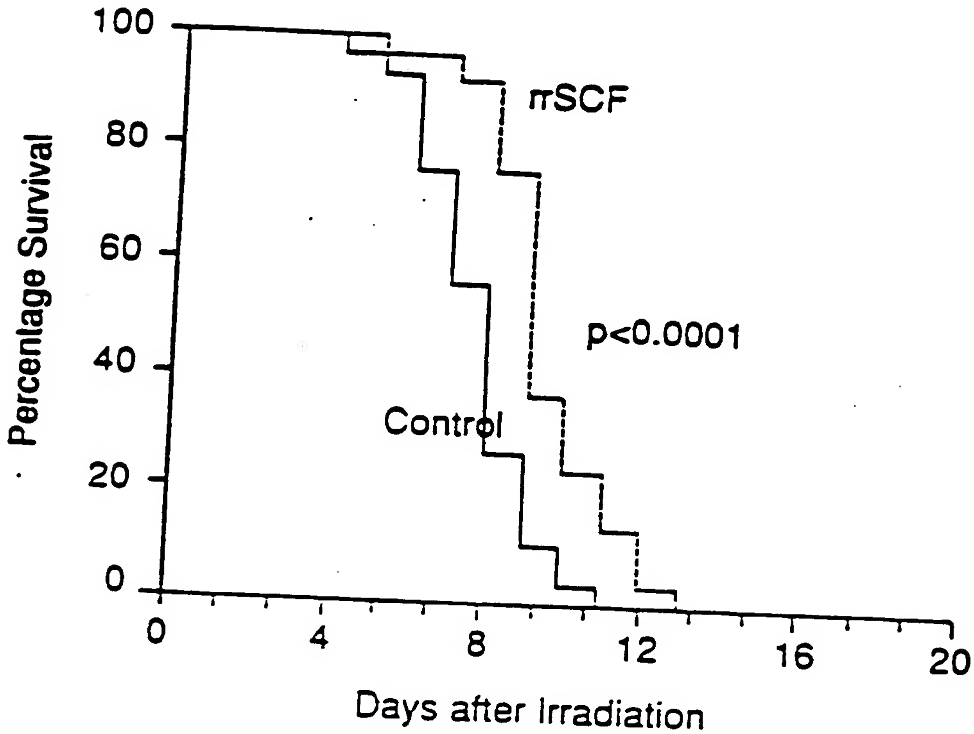
FIG.44B

```
                                        60
Gln Leu Ser Asp Ser Leu Thr Asp Leu Leu Asp Lys Phe Ser Asn
CAA TTG TCA GAC AGC TTG ACT GAT CTT CTG GAC AAG TTT TCA AAT    420

                    70                                  80
Ile Ser Glu Gly Leu Ser Asn Tyr Ser Ile Ile Asp Lys Leu Val
ATT TCT GAA GGC TTG AGT AAT TAT TCC ATC ATA GAC AAA CTT GTG    465

                                        90
Asn Ile Val Asp Asp Leu Val Glu Cys Val Lys Glu Asn Ser Ser
AAT ATA GTG GAT GAC CTT GTG GAG TGC GTG AAA GAA AAC TCA TCT    510

                   100                                 110
Lys Asp Leu Lys Lys Ser Phe Lys Ser Pro Glu Pro Arg Leu Phe
AAG GAT CTA AAA AAA TCA TTC AAG AGC CCA GAA CCC AGG CTC TTT    555

                                       120
Thr Pro Glu Glu Phe Phe Arg Ile Phe Asn Arg Ser Ile Asp Ala
ACT CCT GAA GAA TTC TTT AGA ATT TTT AAT AGA TCC ATT GAT GCC    600

                   130                                 140
Phe Lys Asp Phe Val Val Ala Ser Glu Thr Ser Asp Cys Val Val
TTC AAG GAC TTT GTA GTG GCA TCT GAA ACT AGT GAT TGT GTG GTT    645

                                       150
Ser Ser Thr Leu Ser Pro Glu Lys|Gly|Lys Ala Lys Asn Pro Pro
TCT TCA ACA TTA AGT CCT GAG AAA|GGG|AAG GCC AAA AAT CCC CCT    690
```

FIG.44C

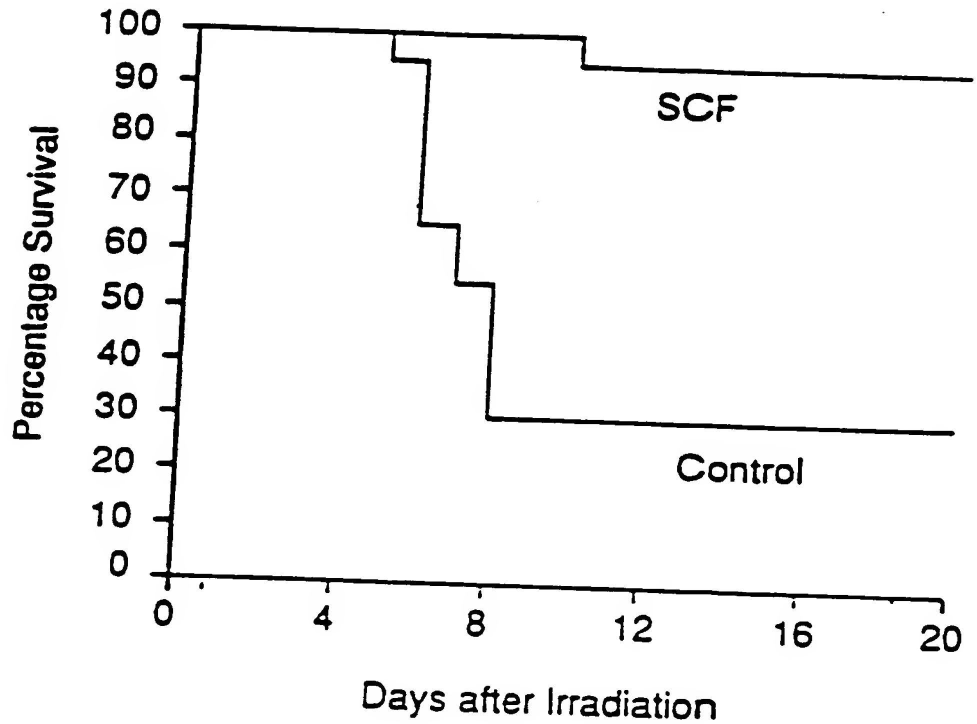
```
                  160                                               170
Gly Asp Ser Ser Leu His Trp Ala Ala Met Ala Leu Pro Ala Leu
GGA GAC TCC AGC CTA CAC TGG GCA GCC ATG GCA TTG CCA GCA TTG    735

                                     180
Phe Ser Leu Ile Ile Gly Phe Ala Phe Gly Ala Leu Tyr Trp Lys
TTT TCT CTT ATA ATT GGC TTT GCT TTT GGA GCC TTA TAC TGG AAG    780

                  190                                       200
Lys Arg Gln Pro Ser Leu Thr Arg Ala Val Glu Asn Ile Gln Ile
AAG AGA CAG CCA AGT CTT ACA AGG GCA GTT GAA AAT ATA CAA ATT    825

                                     210
Asn Glu Glu Asp Asn Glu Ile Ser Met Leu Gln Glu Lys Glu Arg
AAT GAA GAG GAT AAT GAG ATA AGT ATG TTG CAA GAG AAA GAG AGA    870

                  220
Glu Phe Gln Glu Val End
GAG TTT CAA GAA GTG TAA     TTGTGGCTTGTATCAACACTGTTACTTTCGTA    920

CATTGGCTGGTAACAGTTCATGTTTGCTTCATAAATGAAGCAGCTTTAAACAAATTCATA    980

TTCTGTCTGGAGTGACAGACCACATCTTTATCTGTTCTTGCTACCCATGACTTTATATGG 1040

ATGATTCAGAAATTGGAACAGAATGTTTTACTGTGAAACTGGCACTGA             1088
```

FIG.45



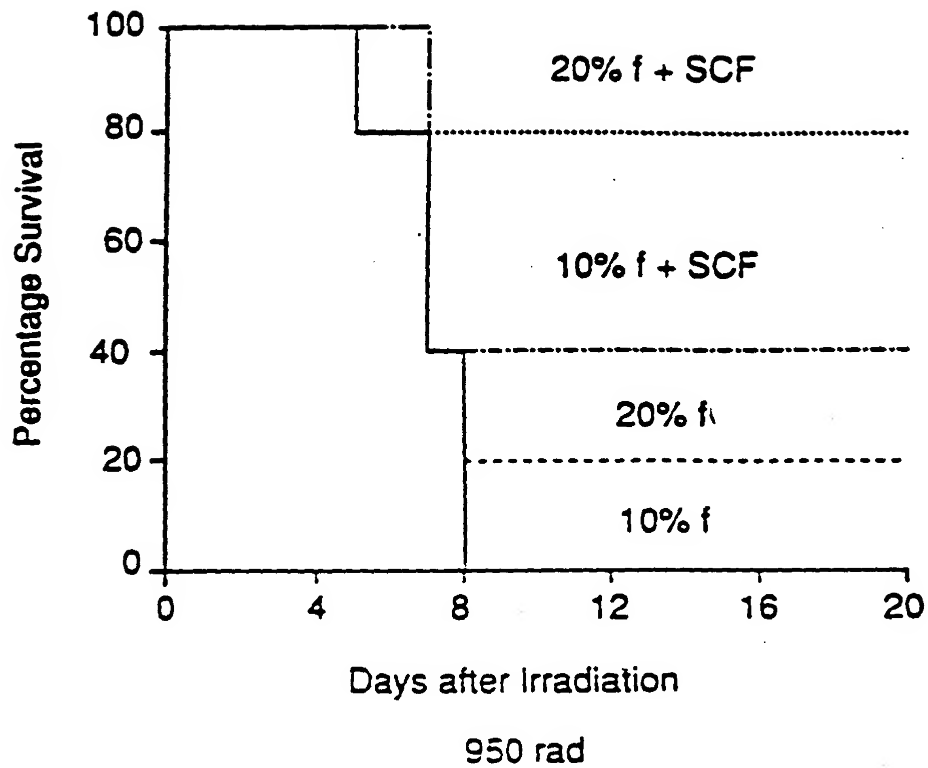
100
80
60
40
20
0
Percentage Survival
rrSCF
p<0.0001
Control
0
4
8
12
16
20
Days after Irradiation

FIG. 46



850 RADS; 5% of femur transplanted

FIG. 47



100
80
60
40
20
0
Percentage Survival
20% f + SCF
10% f + SCF
20% f
10% f
0
4
8
12
16
20
Days after Irradiation
950 rad

FIG. 48

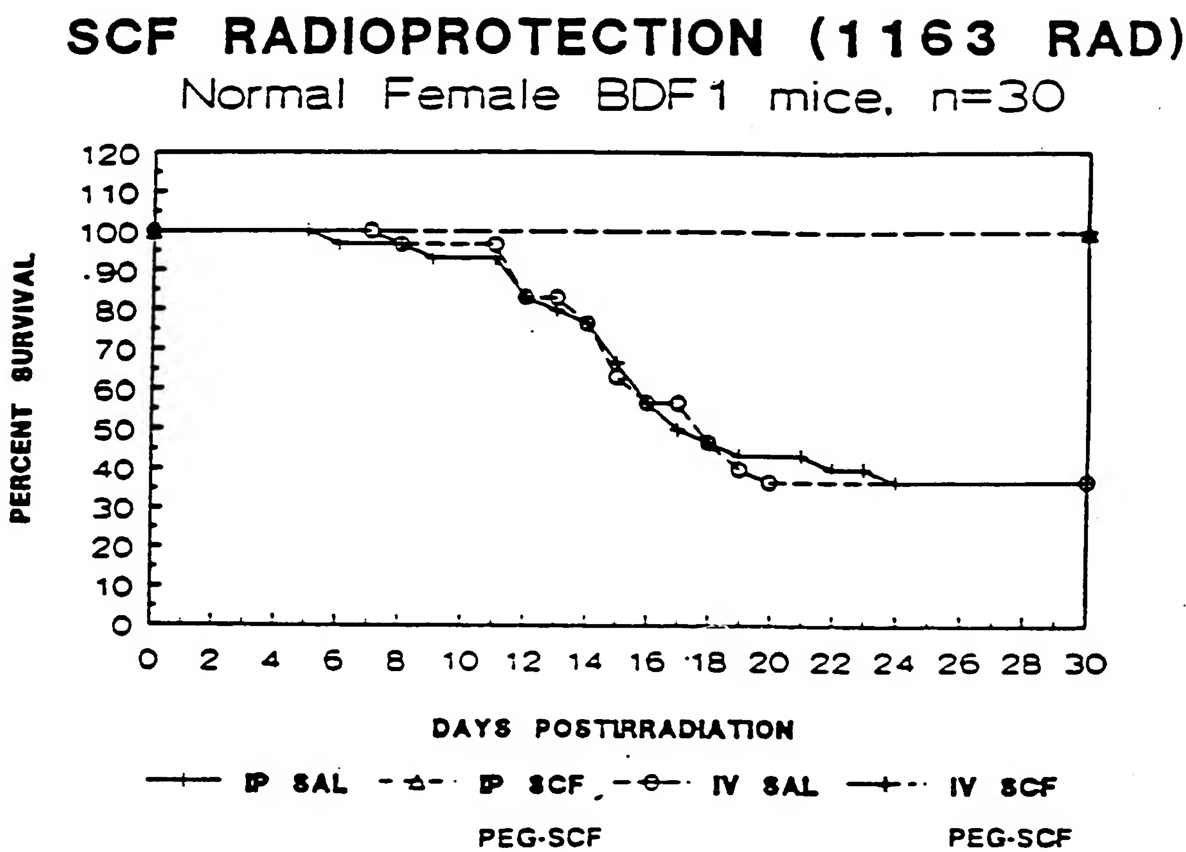

SCF RADIOPROTECTION (1163 RAD)
Normal Female BDF1 mice, n=30
PERCENT SURVIVAL
120
110
100
90
80
70
60
50
40
30
20
10
0
0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30
DAYS POSTIRRADIATION
IP SAL
IP SCF
PEG-SCF
IV SAL
IV SCF
PEG-SCF

FIG. 49

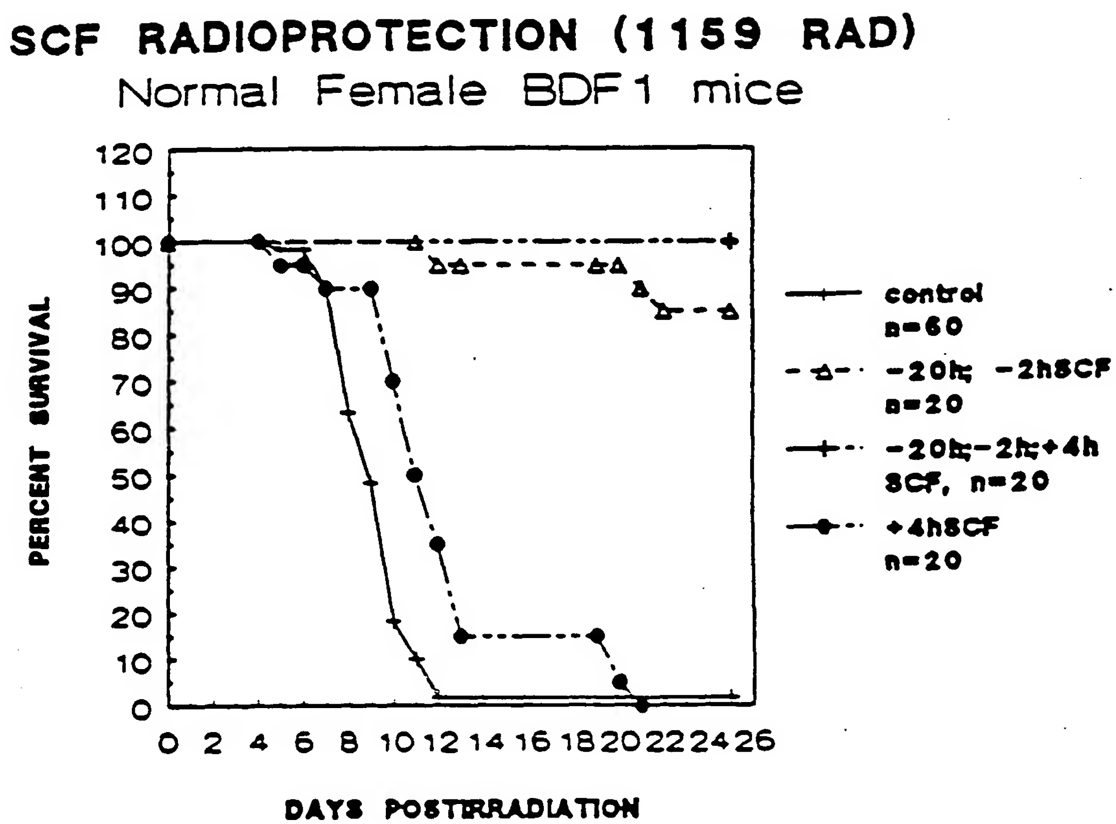
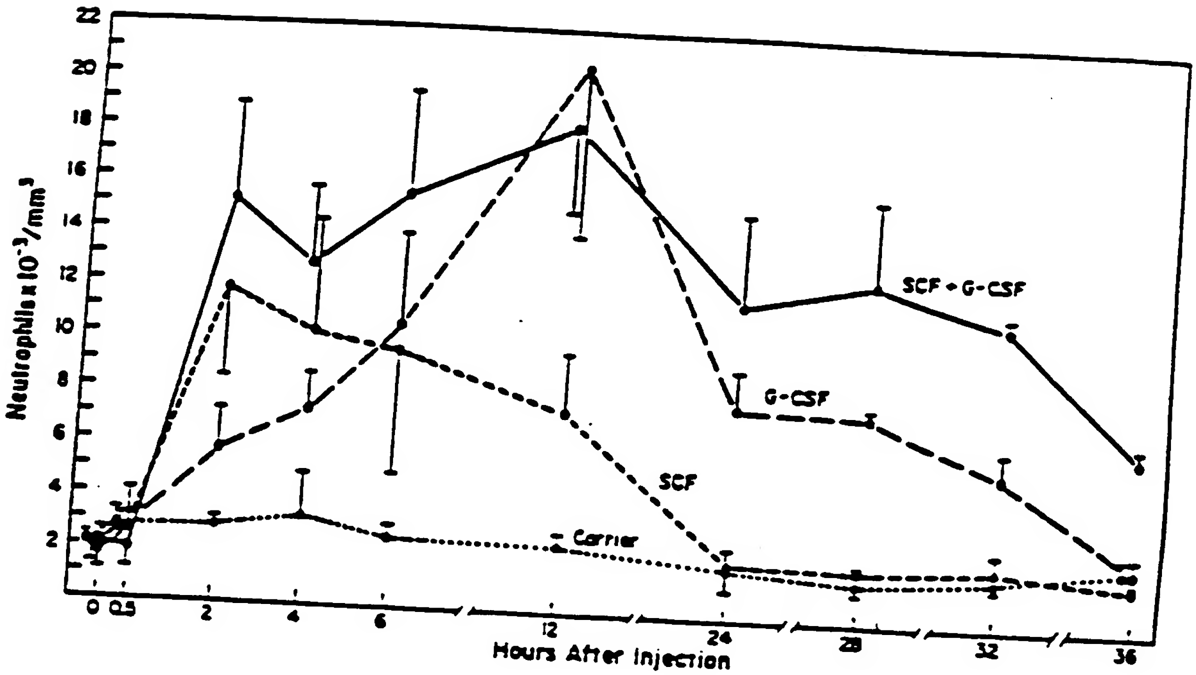
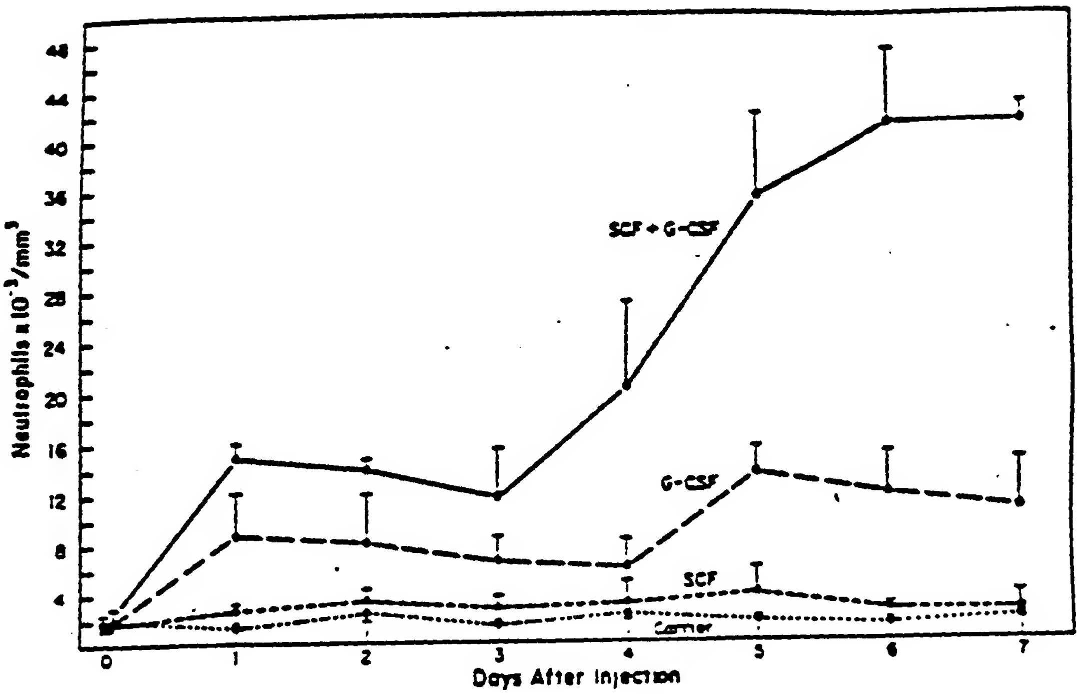

SCF RADIOPROTECTION (1159 RAD)
Normal Female BDF1 mice
PERCENT SURVIVAL
0
10
20
30
40
50
60
70
80
90
100
110
120
0 2 4 6 8 10 12 14 16 18 20 22 24 26
DAYS POSTIRRADIATION
control
n=60
-20h; -2hSCF
n=20
-20h;-2h;+4h
SCF, n=20
+4hSCF
n=20

FIG. 50



Neutrophils x 10^-3/mm^3
22
20
18
16
14
12
10
8
6
4
2
SCF + G-CSF
G-CSF
SCF
Carrier
0
0.5
2
4
6
12
24
28
32
36
Hours After Injection

FIG. 51



Neutrophils x 10⁻³/mm³
48
44
40
36
32
28
24
20
16
12
8
4
SCF + G-CSF
G-CSF
SCF
Carrier
0
1
2
3
4
5
6
7
Days After Injection

FIG. 52

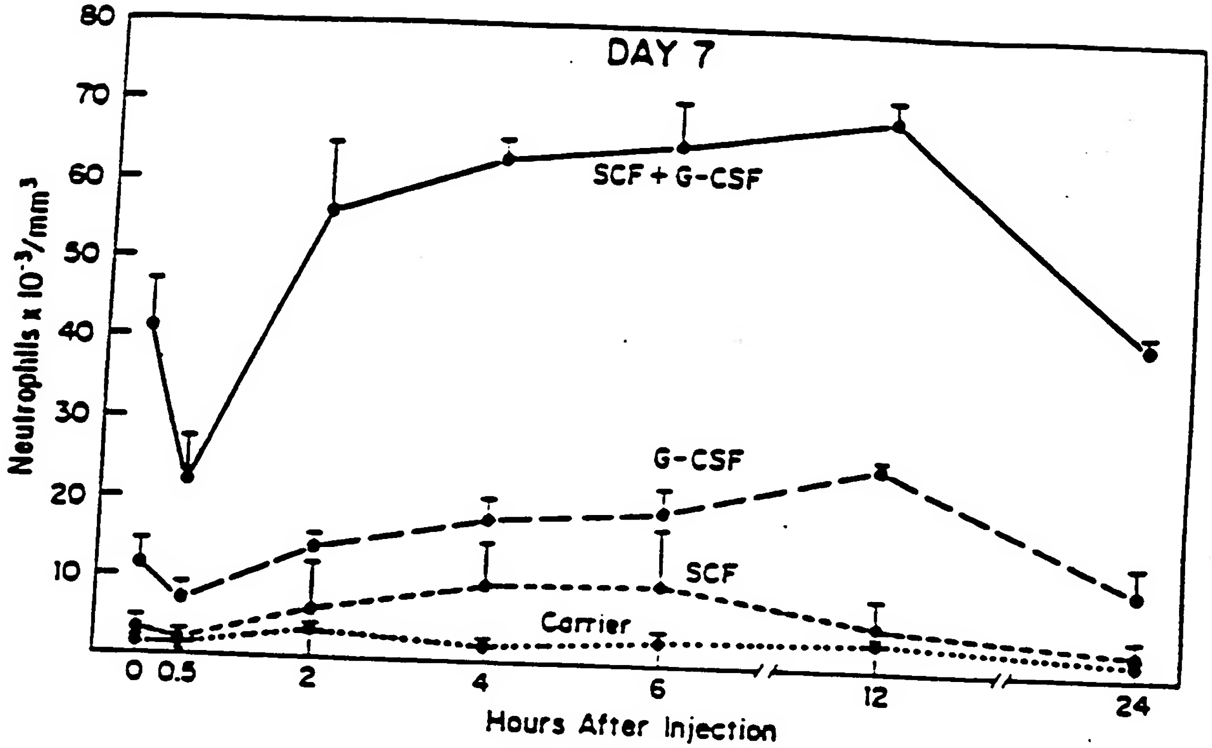

DAY 7
SCF + G-CSF
G-CSF
SCF
Carrier
Neutrophils x 10^{-3}/mm^3
80
70
60
50
40
30
20
10
0
0.5
2
4
6
12
24
Hours After Injection

FIG. 53

in vivo Administration of SCF–Platelet Counts

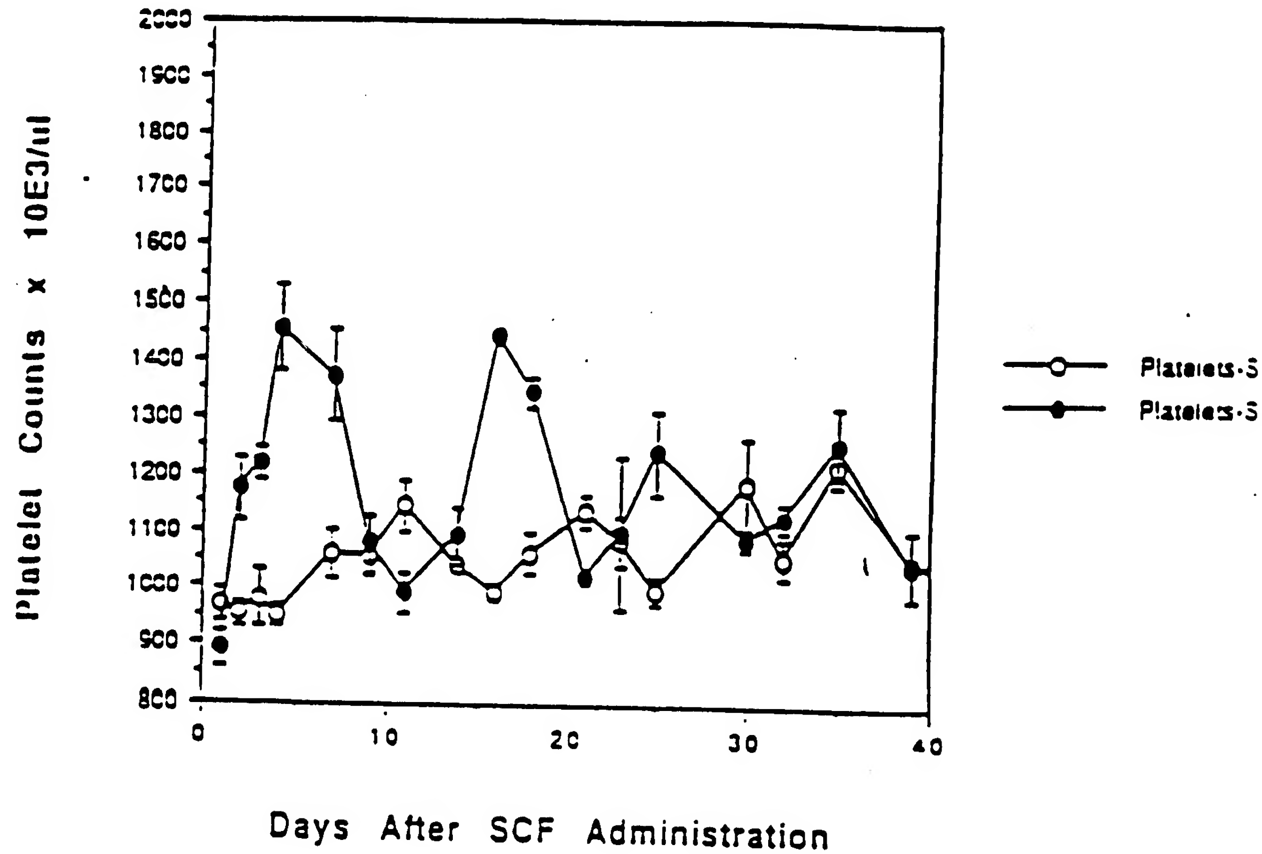


FIG. 54

Dose/Response of rrSCF-PEG on Platelet Counts

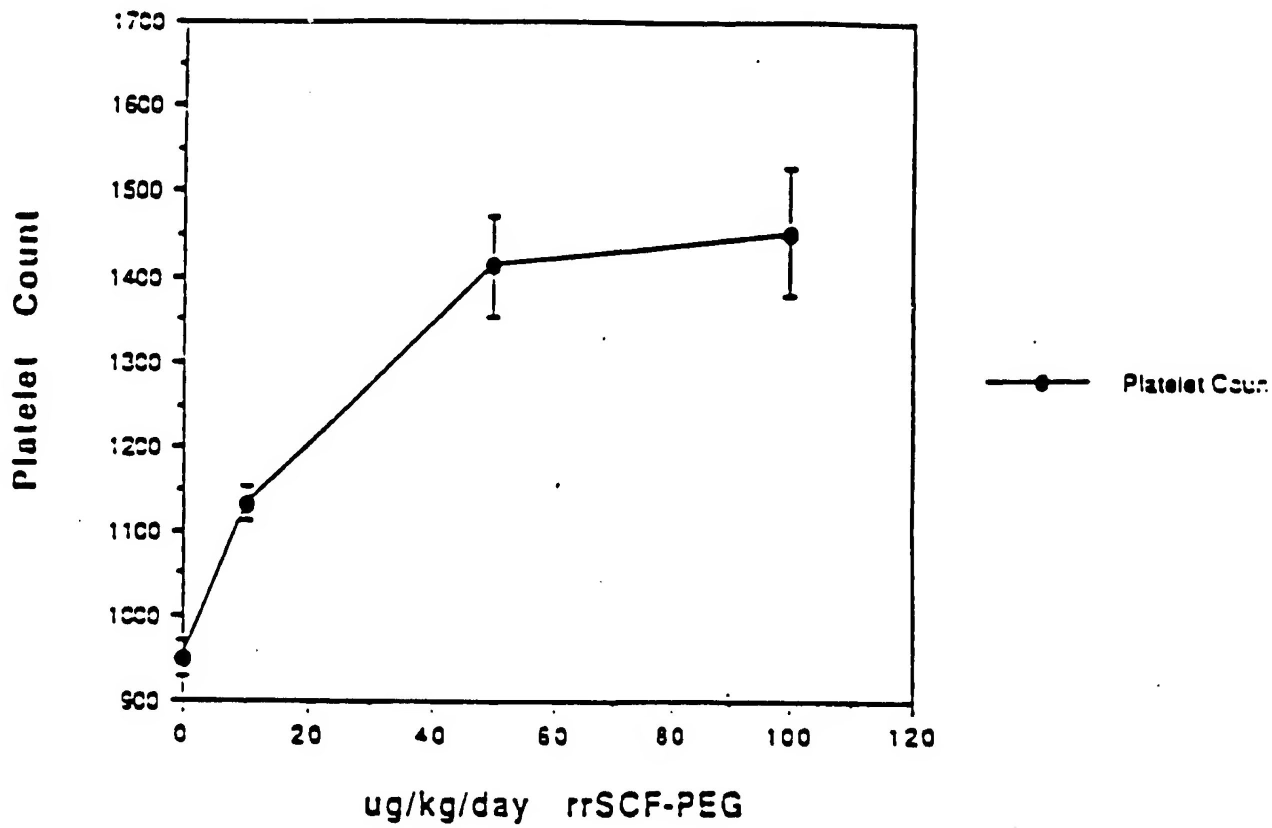
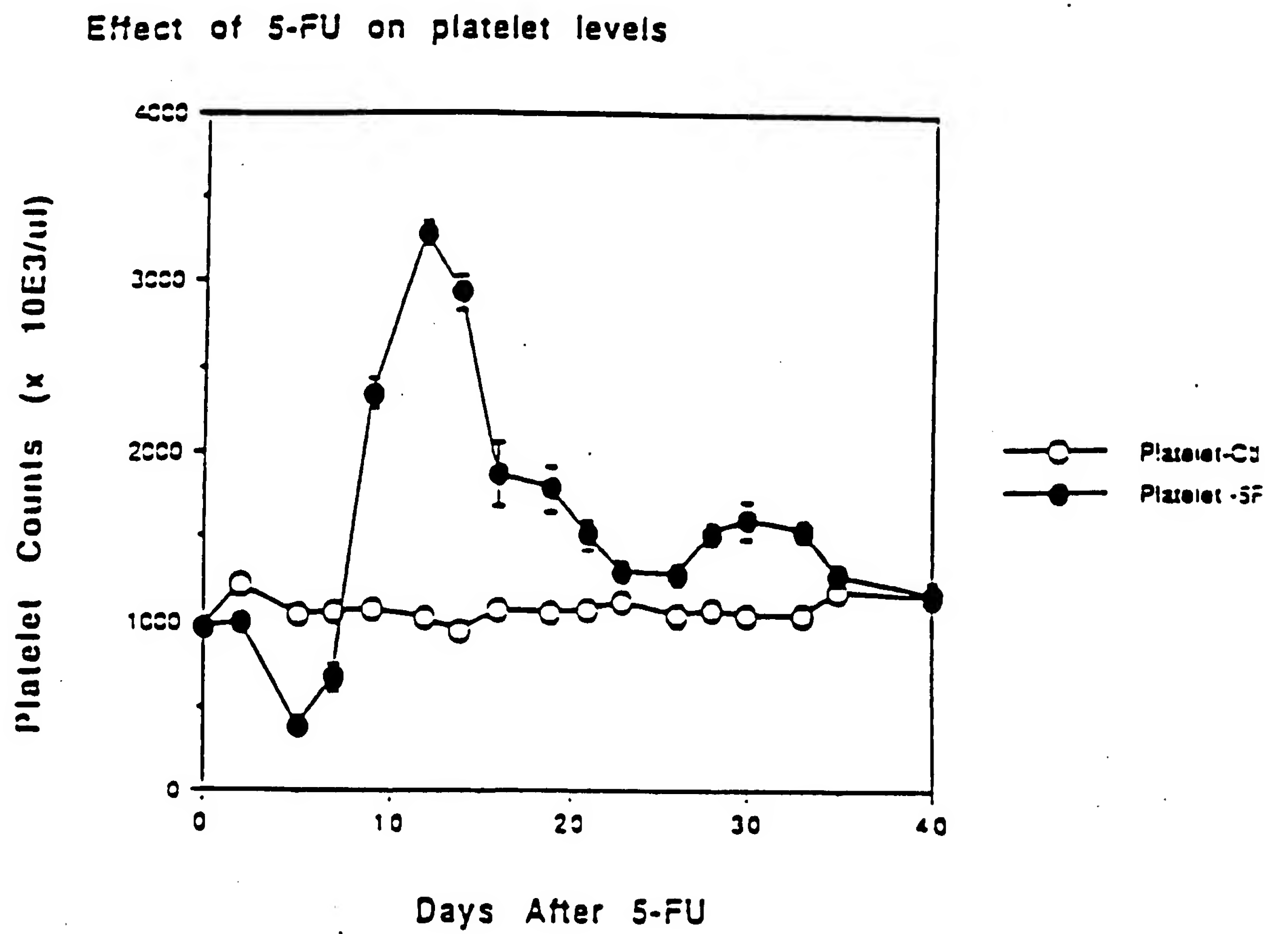


FIG. 55

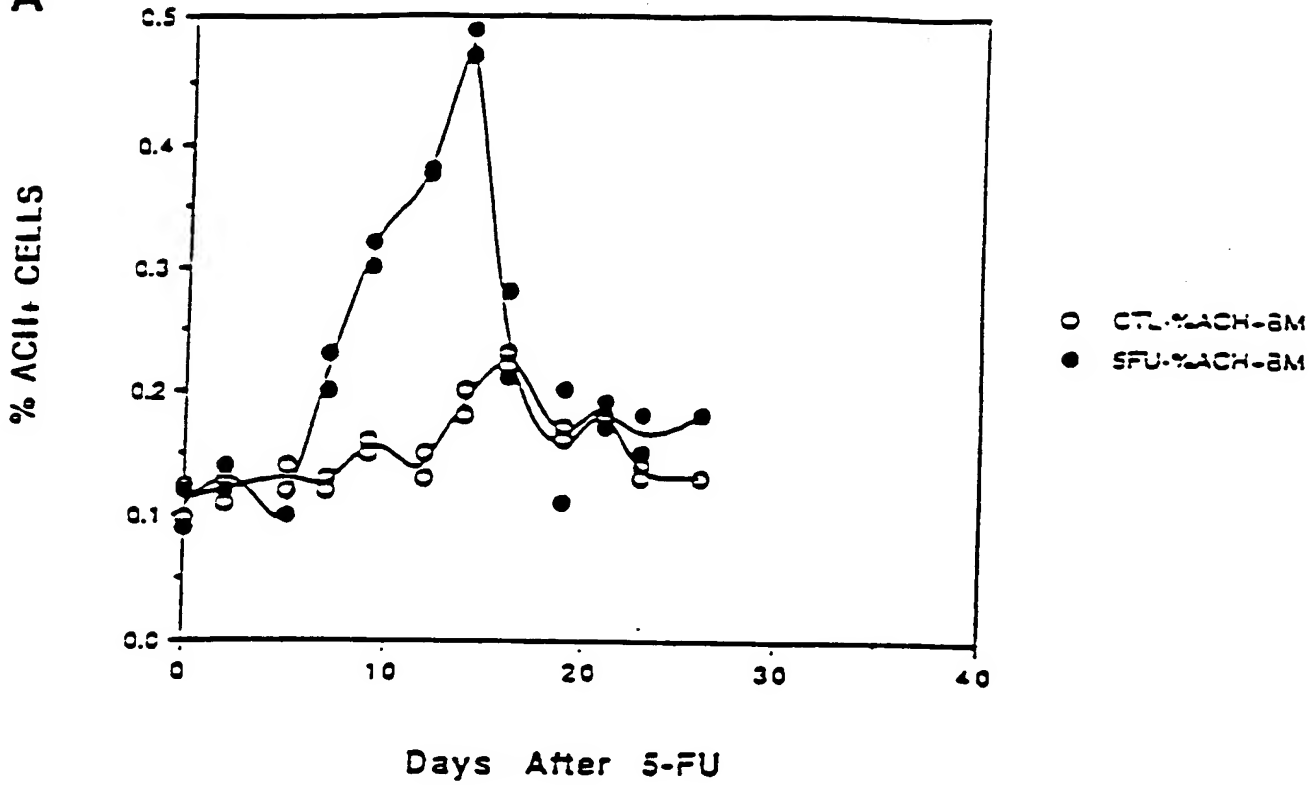


Effect of 5-FU on platelet levels
Platelet Counts (x 10E3/ul)
4000
3000
2000
1000
0
0
10
20
30
40
Days After 5-FU
Platelet-Ct
Platelet -5F

FIG. 56

5-FU Effect on ACH+ Cells in Marrow

A



5-FU Effect on ACH+ Cells in Spleen

B

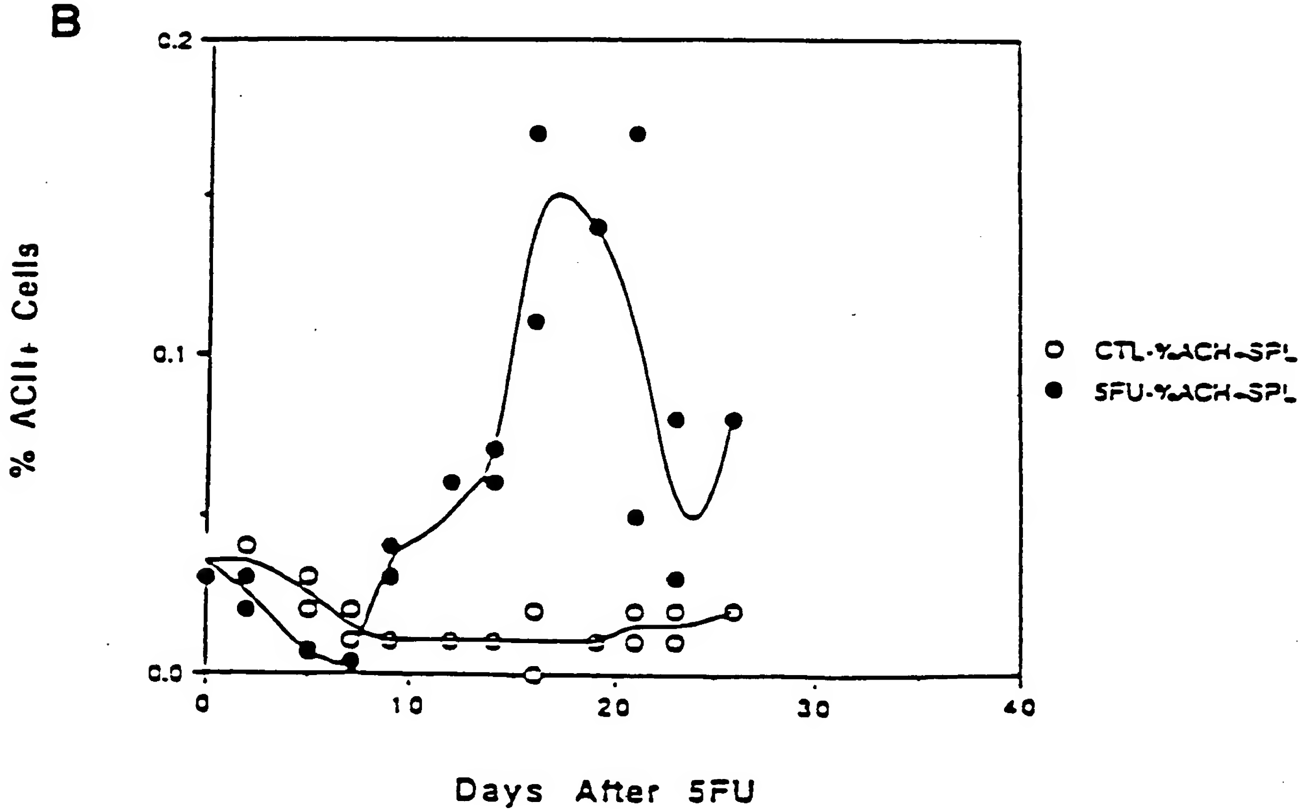
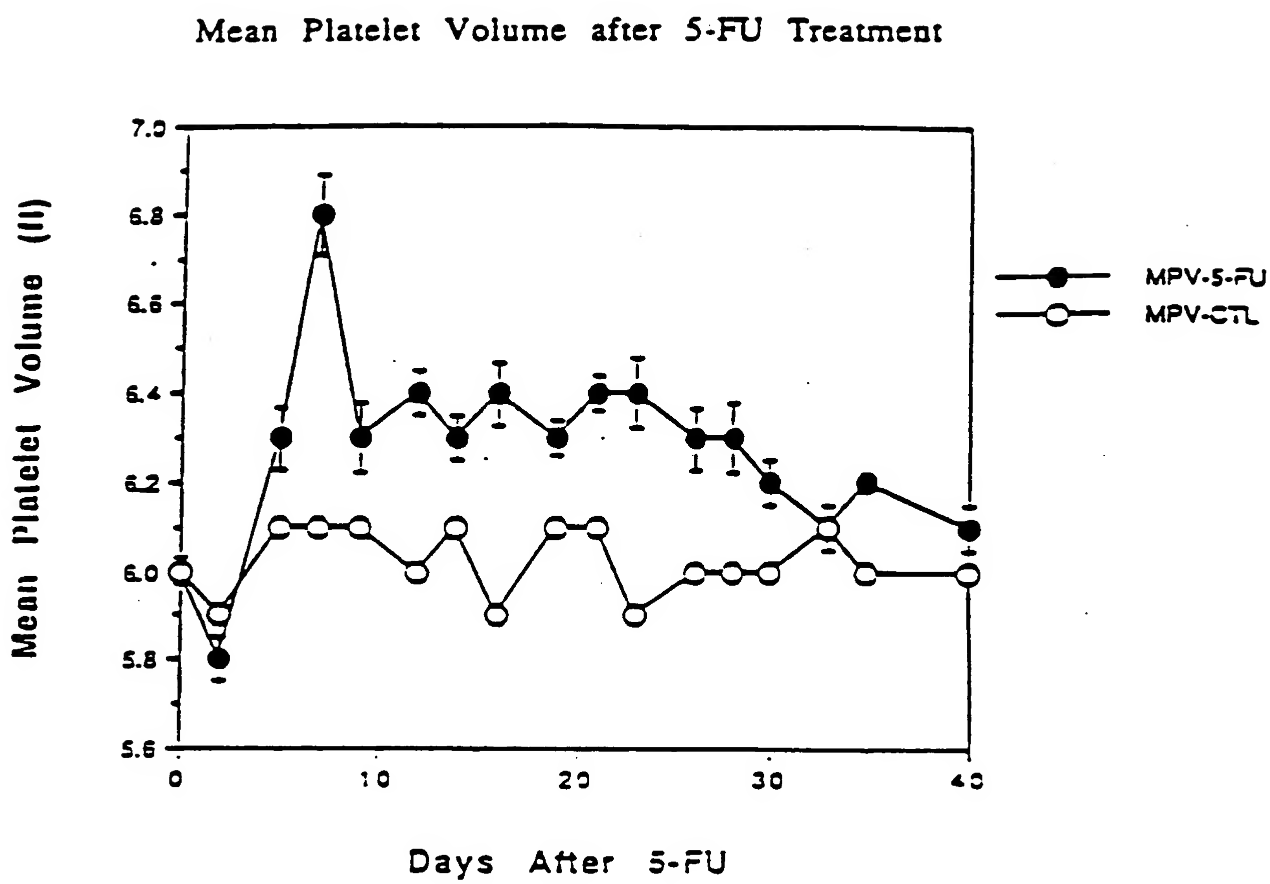


FIG. 57



Mean Platelet Volume after 5-FU Treatment
7.0
6.8
6.6
6.4
6.2
6.0
5.8
5.6
0
10
20
30
40
Mean Platelet Volume (fl)
Days After 5-FU
MPV-5-FU
MPV-CTL

FIG. 58

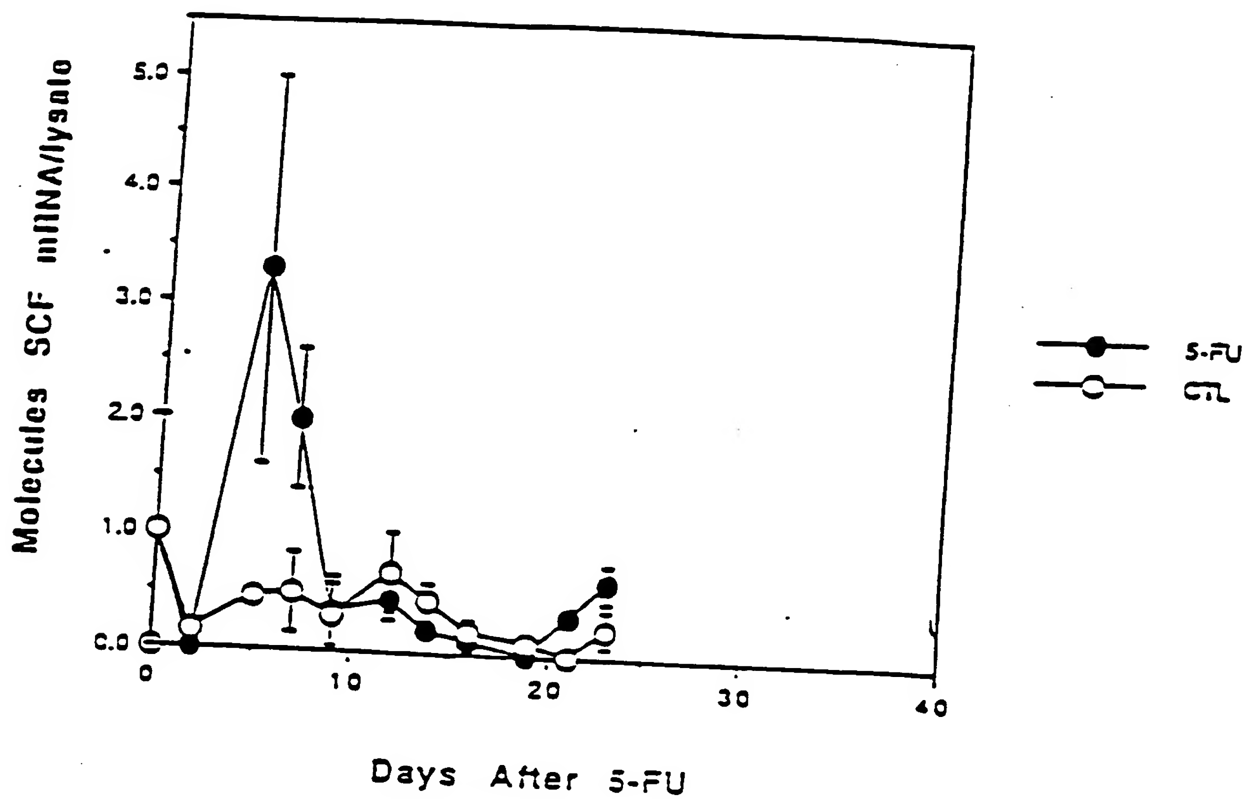

Molecules SCF mRNA/lysate
5.0
4.0
3.0
2.0
1.0
0.0
0
10
20
30
40
Days After 5-FU
5-FU
CTL

FIG. 59

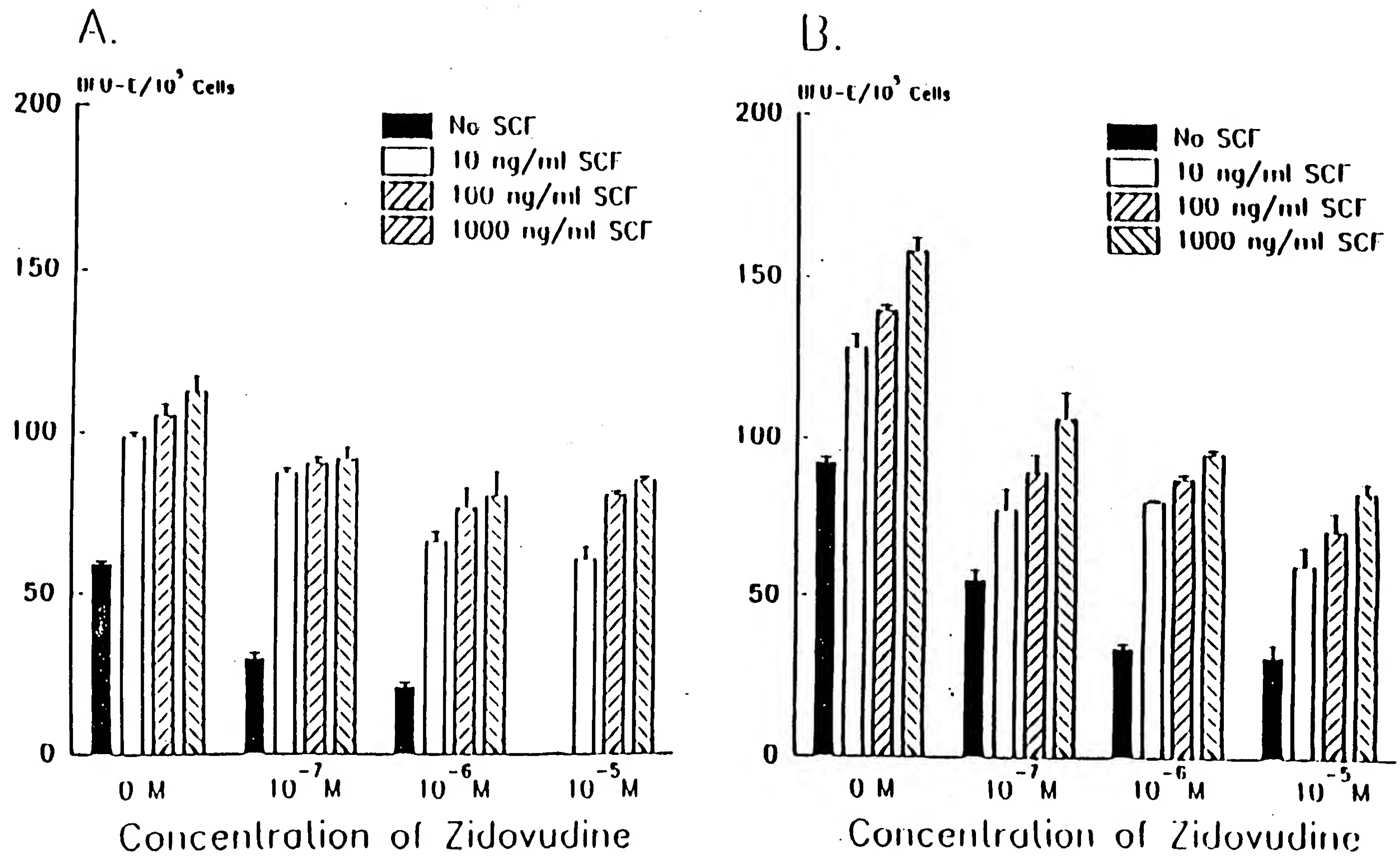
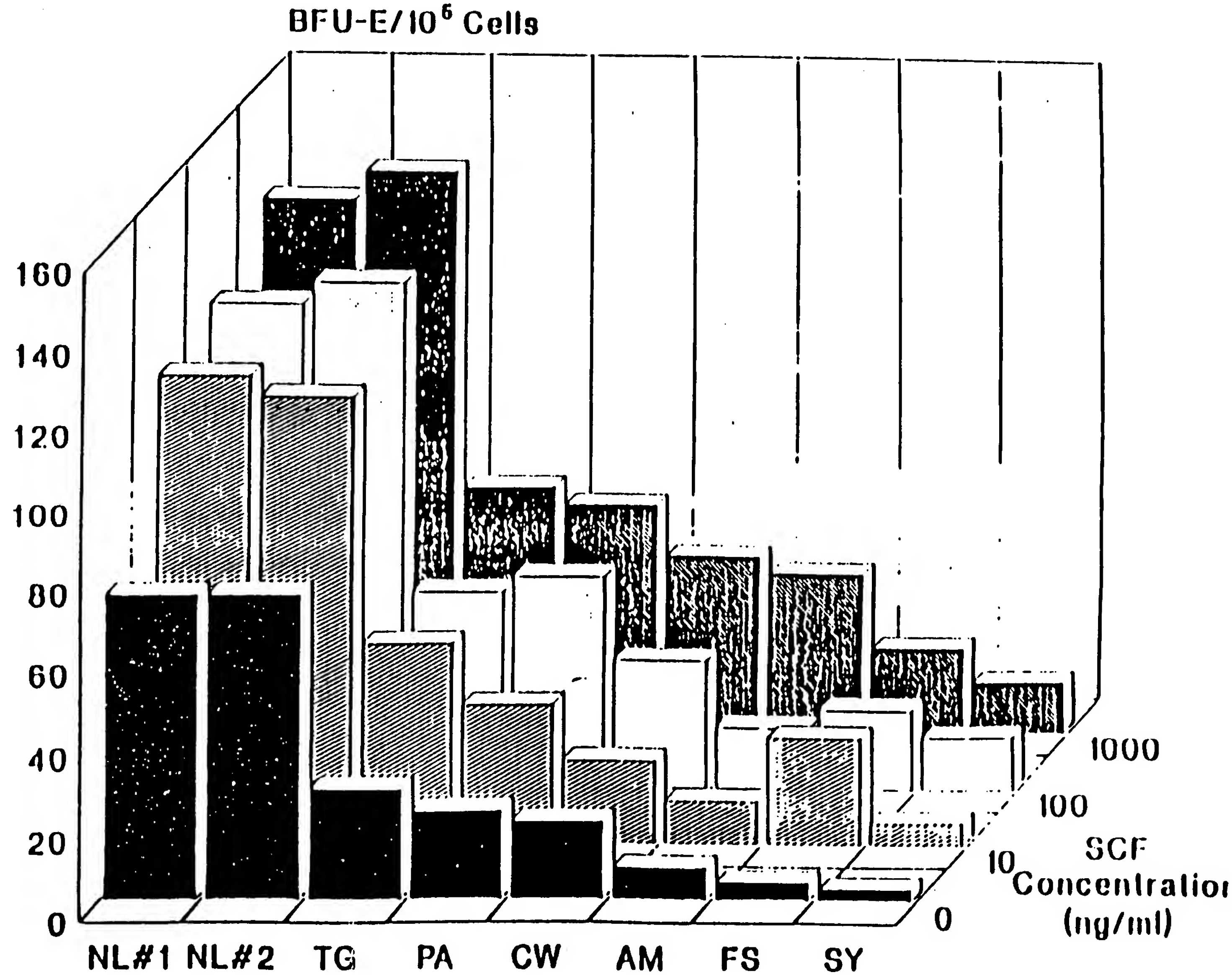

A.
B.
BFU-E/10⁵ Cells
200
150
100
50
0
No SCF
10 ng/ml SCF
100 ng/ml SCF
1000 ng/ml SCF
0 M
10^-7 M
10^-6 M
10^-5 M
Concentration of Zidovudine

FIG. 60



BFU-E/10^6 Cells
160
140
120
100
80
60
40
20
0
NL#1
NL#2
TG
PA
CW
AM
FS
SY
0
10
100
1000
SCF
Concentration
(ng/ml)

FIG. 61

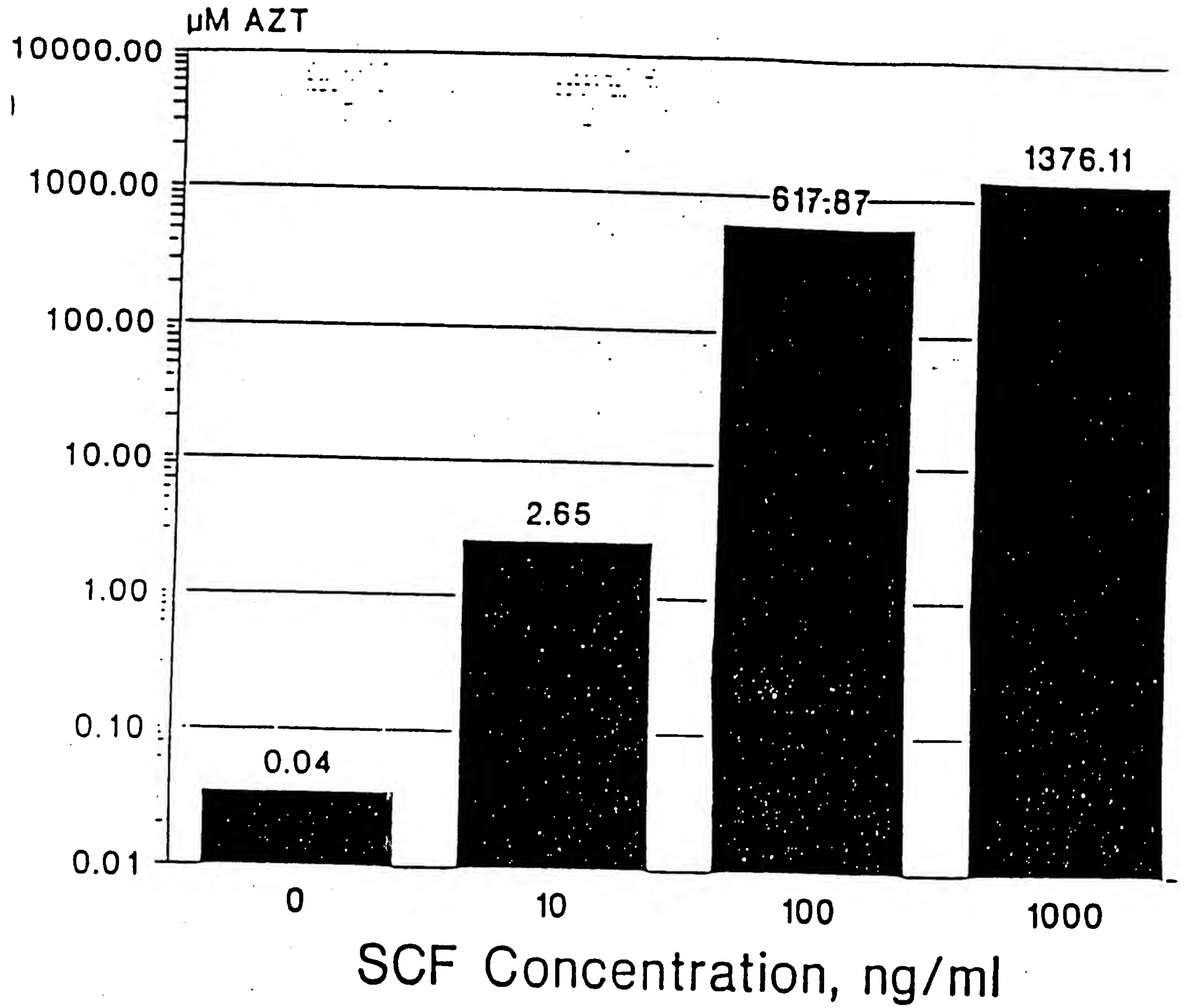

µM AZT
10000.00
1000.00
100.00
10.00
1.00
0.10
0.01
0.04
2.65
617.87
1376.11
0
10
100
1000
SCF Concentration, ng/ml

FIG. 62

EFFECT OF SCF ON AZT SUPPRESSION OF BMC

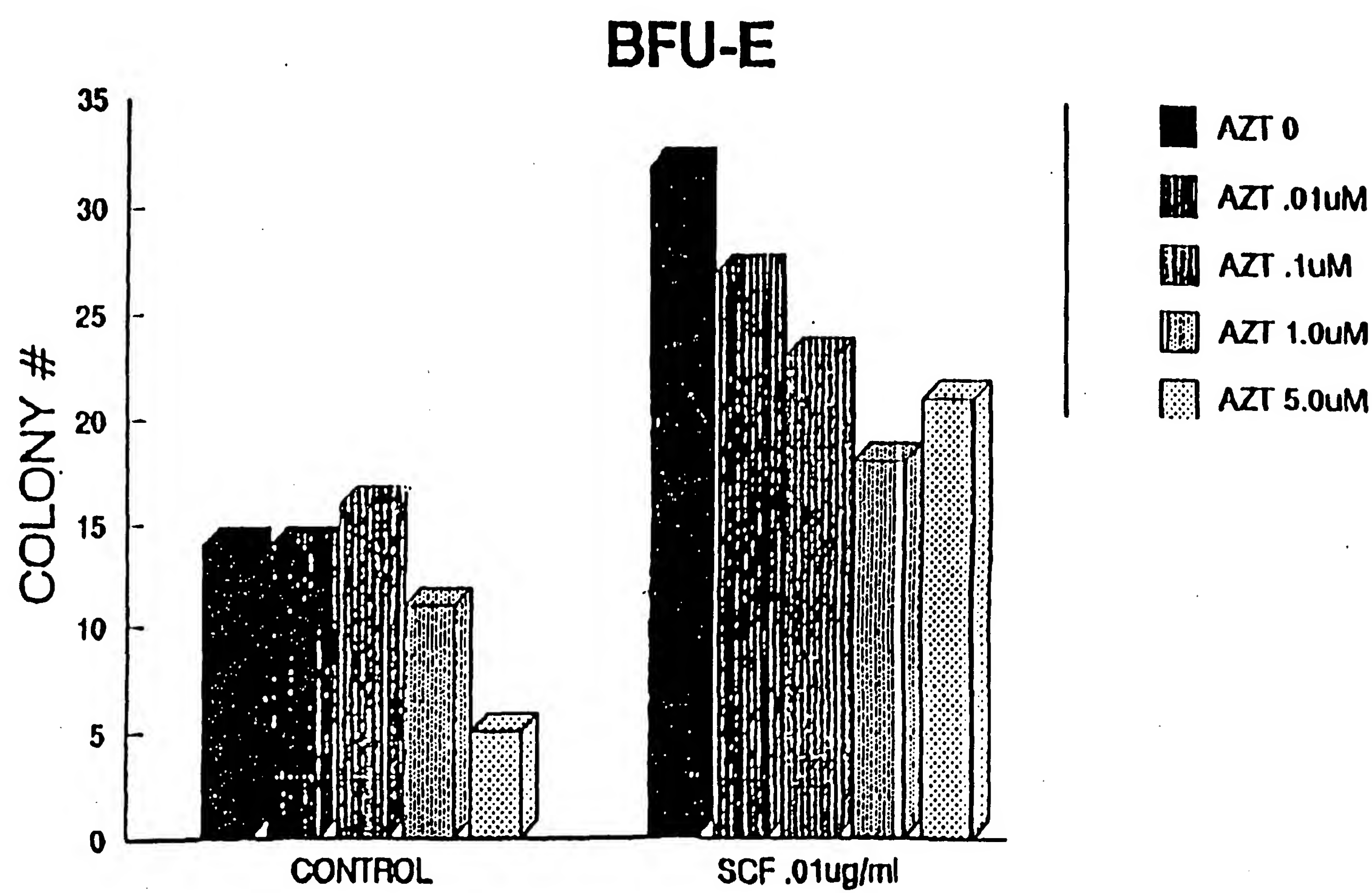


FIG. 63

EFFECT OF SCF ON AZT SUPPRESSION OF BMC

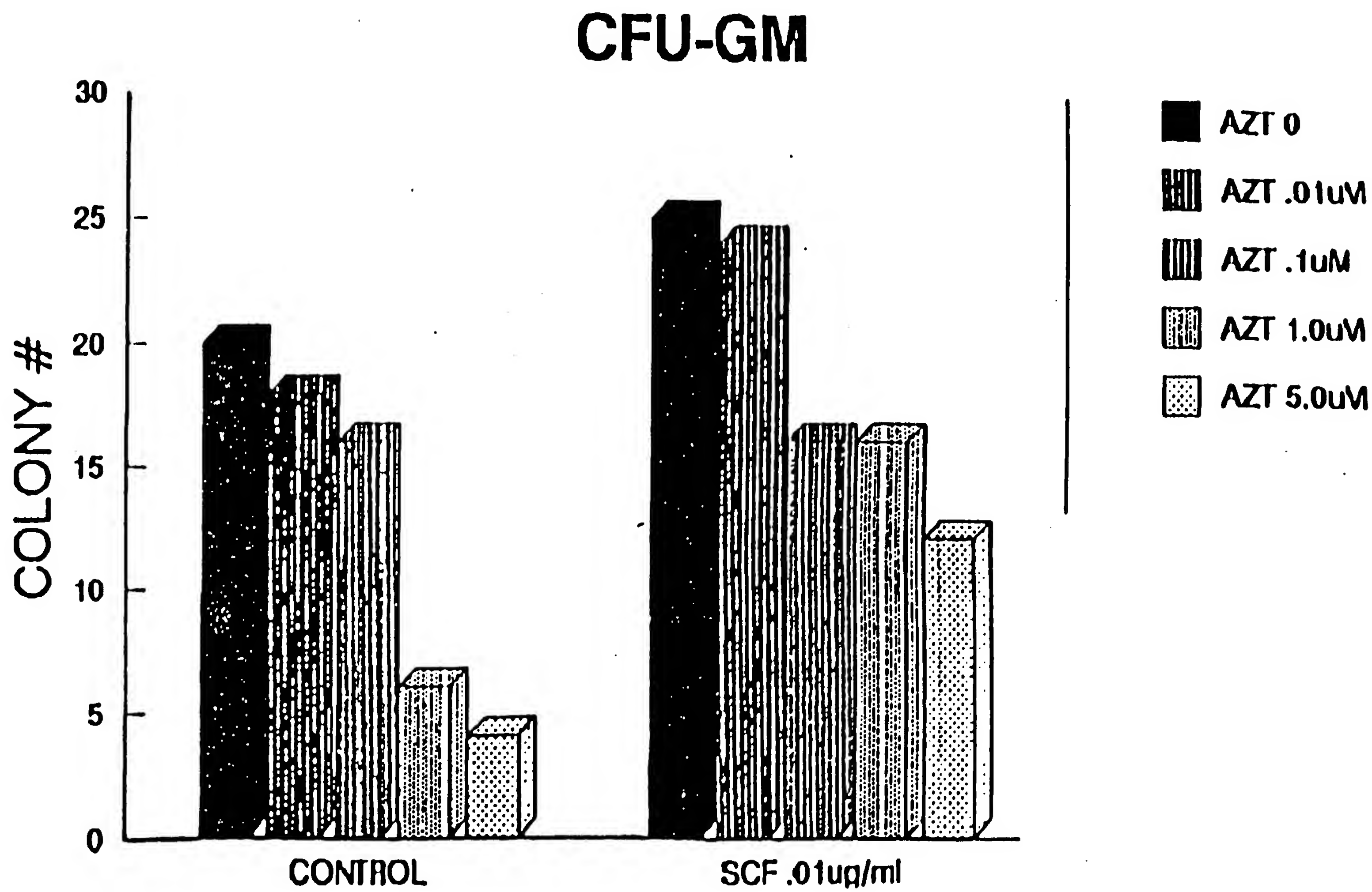


FIG. 64

EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC

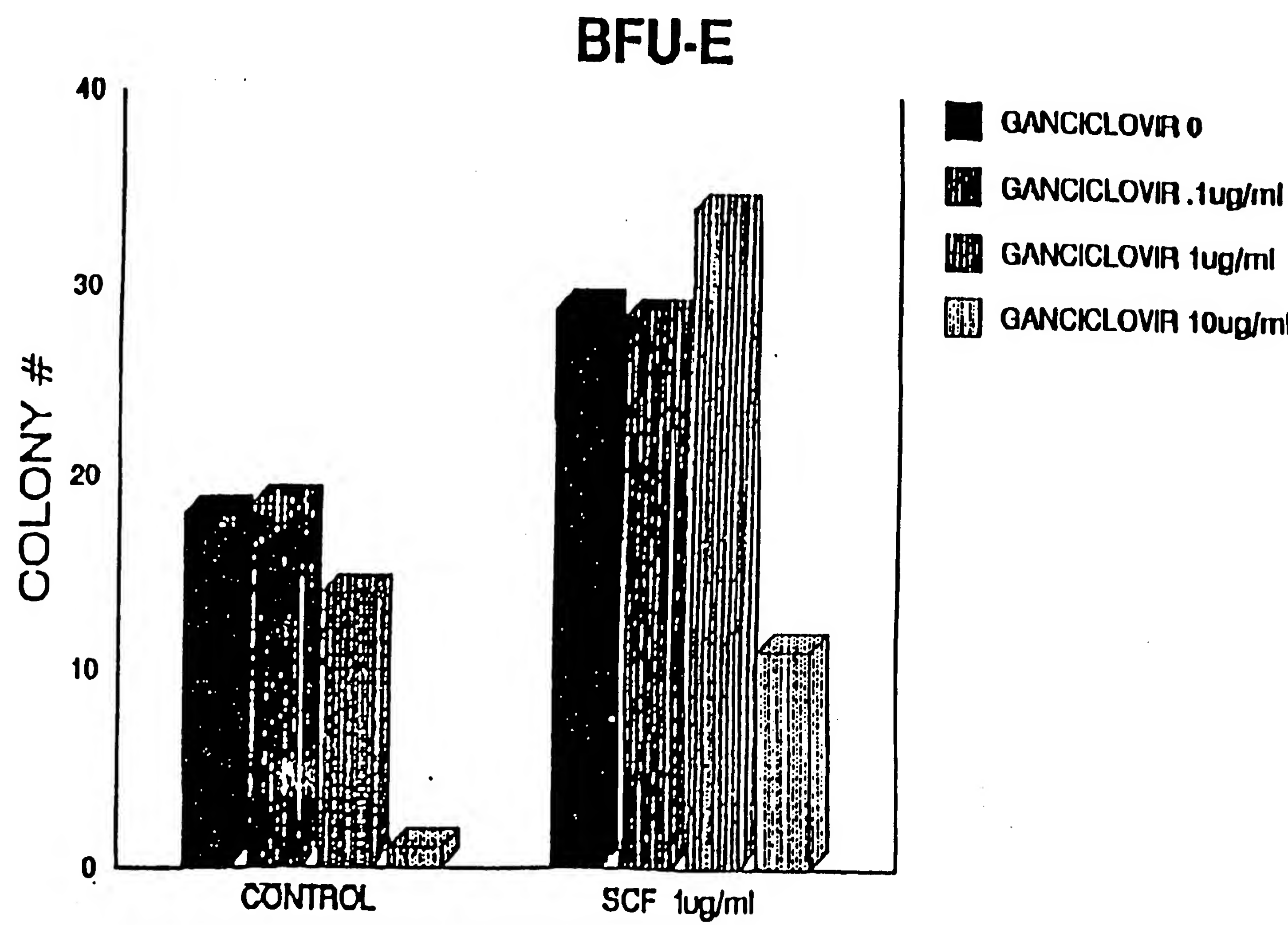


FIG. 65

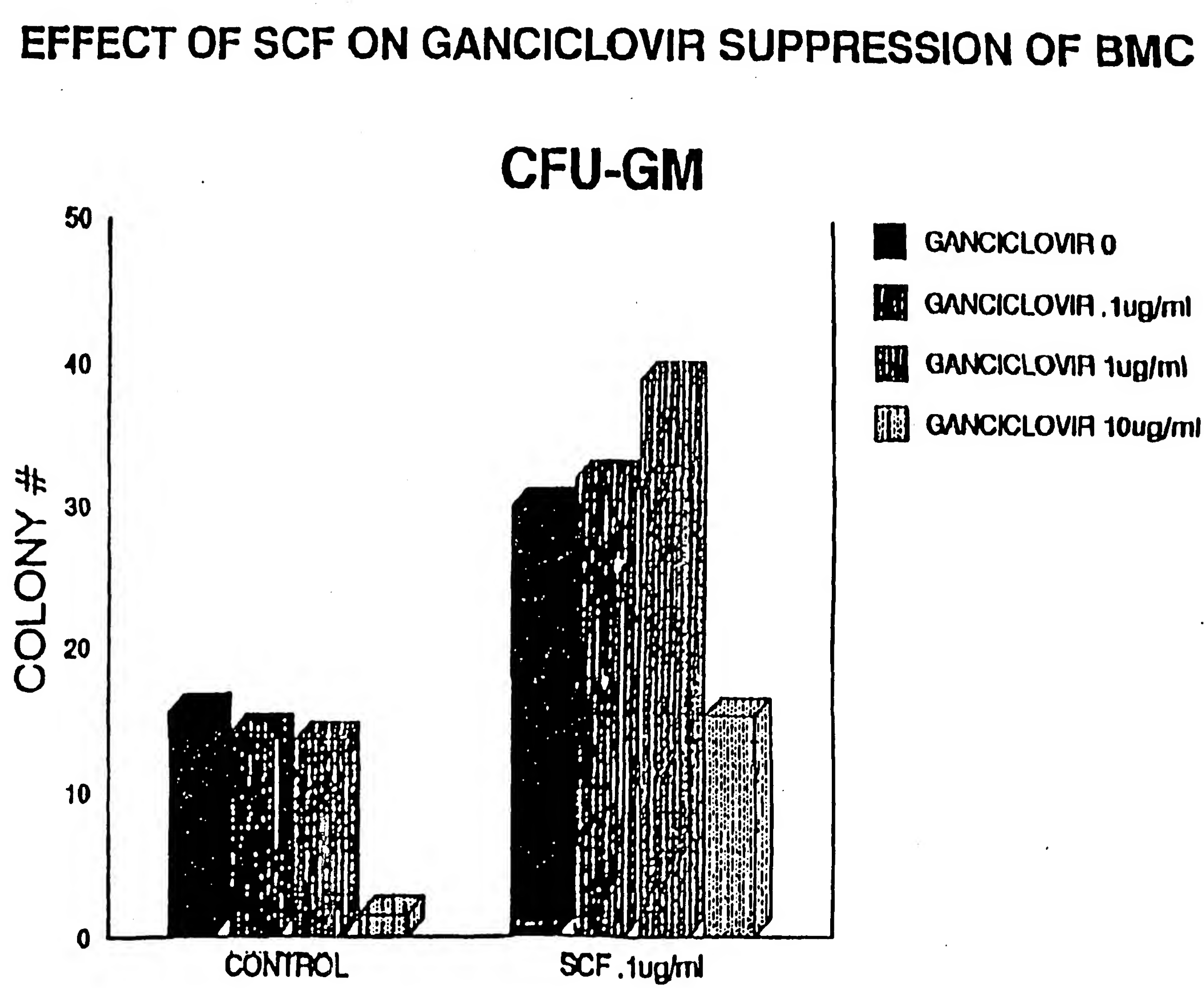

EFFECT OF SCF ON GANCICLOVIR SUPPRESSION OF BMC
CFU-GM
COLONY #
50
40
30
20
10
0
CONTROL
SCF .1ug/ml
GANCICLOVIR 0
GANCICLOVIR .1ug/ml
GANCICLOVIR 1ug/ml
GANCICLOVIR 10ug/ml

FIG. 66

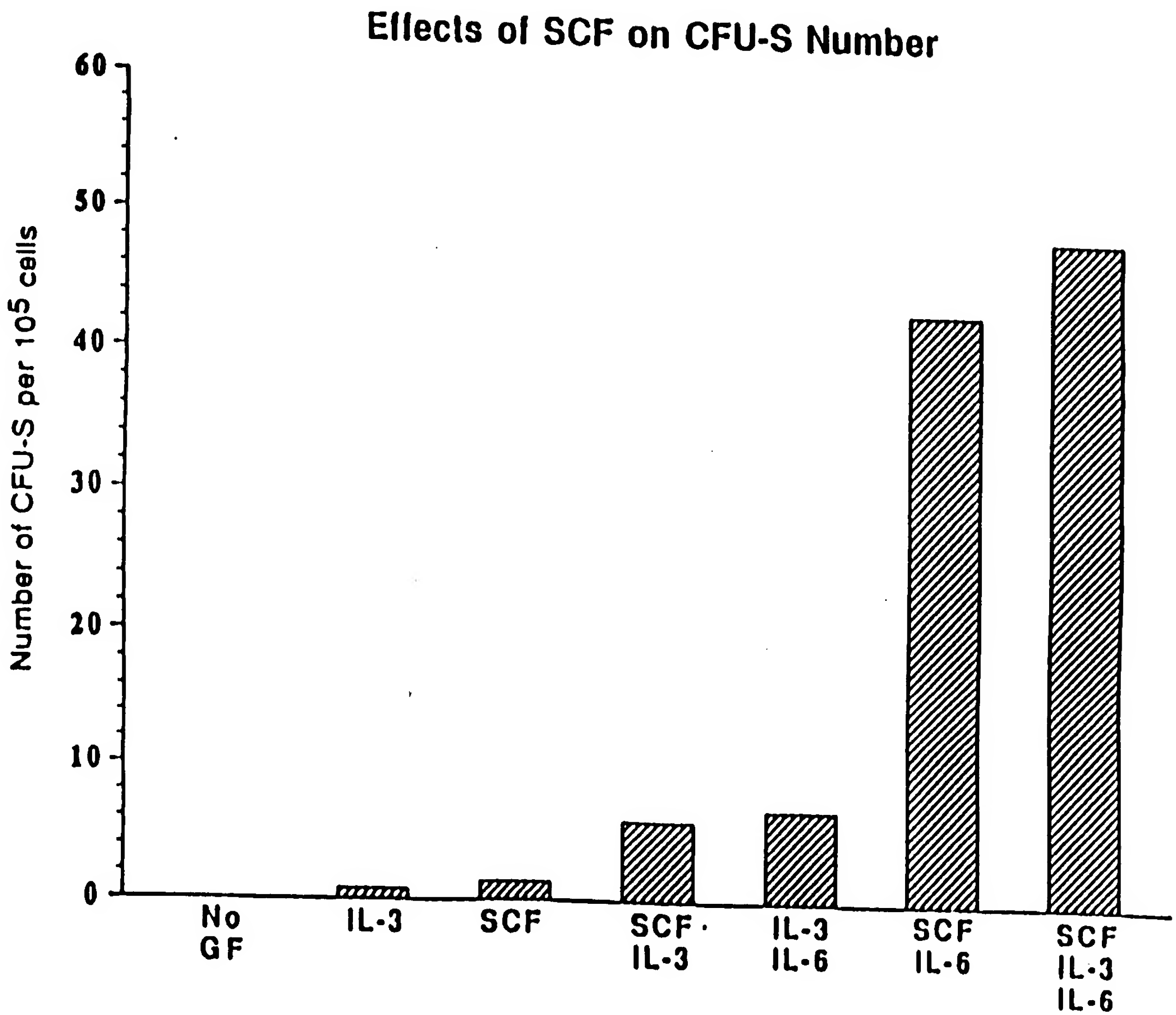

Effects of SCF on CFU-S Number
Number of CFU-S per 10^5 cells
60
50
40
30
20
10
0
No GF
IL-3
SCF
SCF IL-3
IL-3 IL-6
SCF IL-6
SCF IL-3 IL-6

FIG. 67

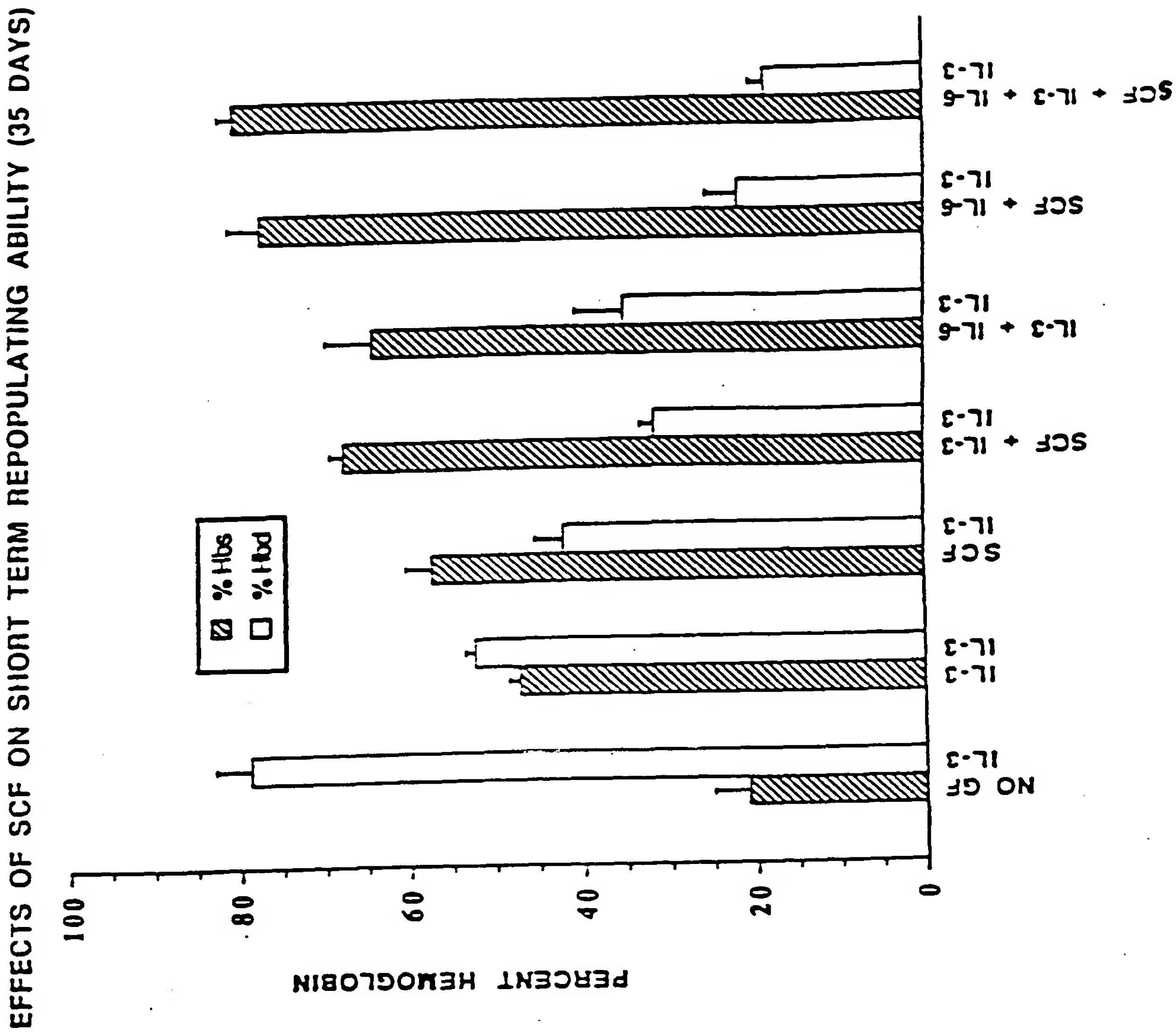
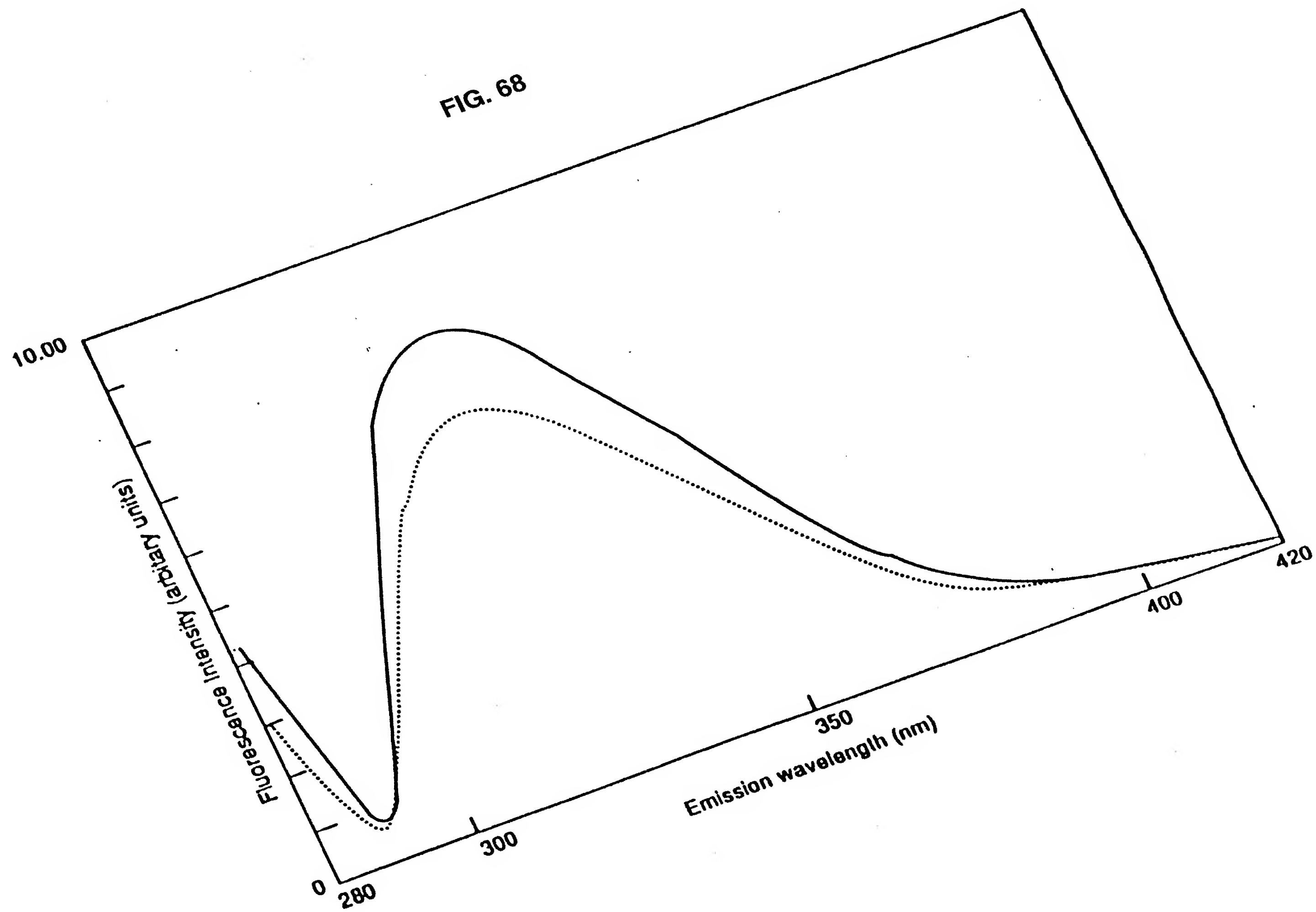

EFFECTS OF SCF ON SHORT TERM REPOPULATING ABILITY (35 DAYS)
PERCENT HEMOGLOBIN
100
80
60
40
20
0
% Hbs
% Hbd
NO GF
IL-3
IL-3
IL-3
SCF
IL-3
SCF + IL-3
IL-3
IL-3 + IL-6
IL-3
SCF + IL-6
IL-3
SCF + IL-3 + IL-6
IL-3

FIG. 68



10.00
0
Fluorescence Intensity (arbitary units)
280
300
350
400
420
Emission wavelength (nm)

FIG. 69A

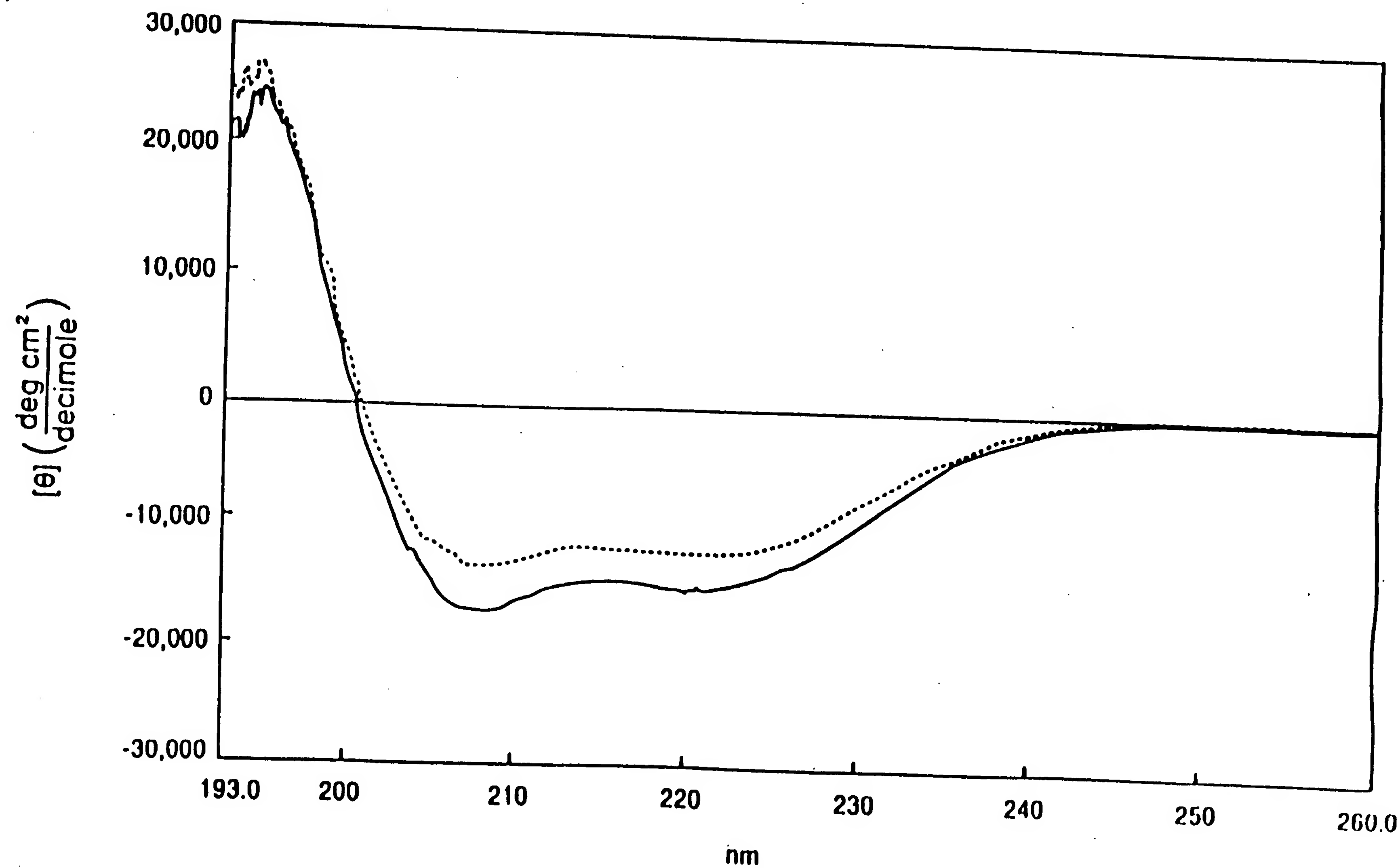
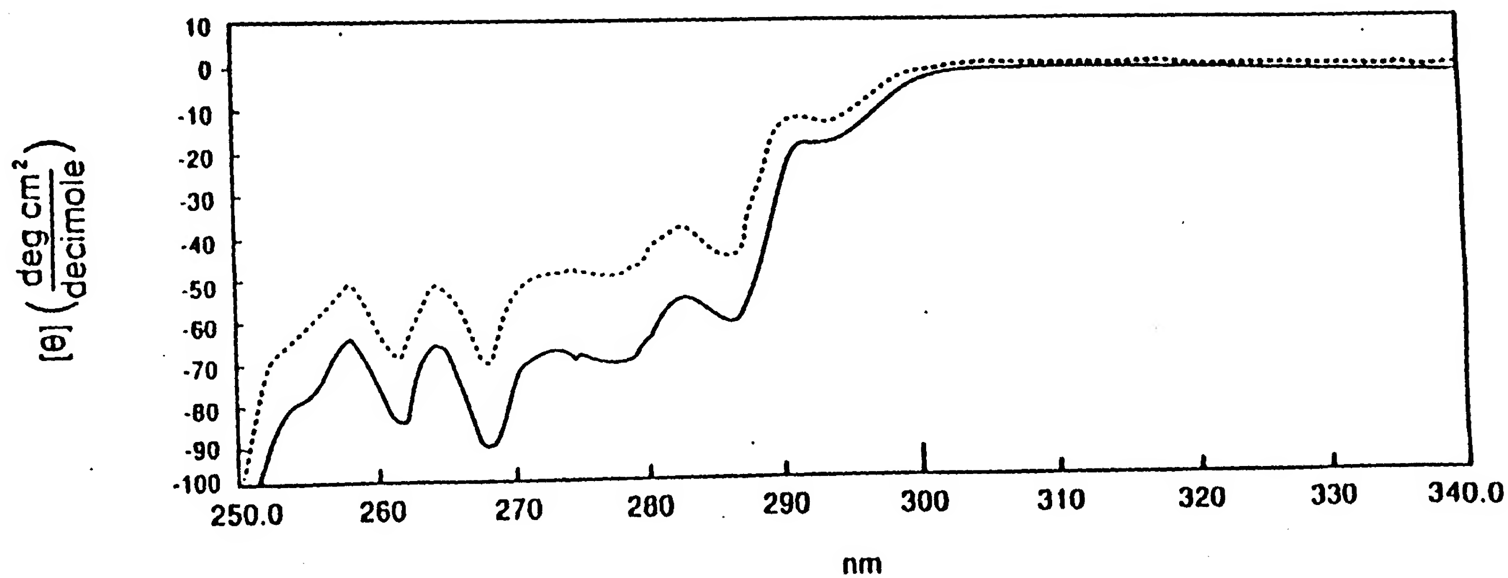

30,000
20,000
10,000
0
-10,000
-20,000
-30,000
[θ] (deg cm² / decimole)
193.0
200
210
220
230
240
250
260.0
nm

FIG. 69B



[θ] $\left(\frac{\text{deg cm}^2}{\text{decimole}}\right)$
10
0
-10
-20
-30
-40
-50
-60
-70
-80
-90
-100
250.0
260
270
280
290
300
310
320
330
340.0
nm

FIG. 70